### Yaen, Christopher

From:

Sent:

Yaen, Christopher Tuesday, April 23, 2002 5:07 PM STIC-Biotech/ChemLib

To:

Subject:

09689469

could you please do a seq search on seq id no: 3-6 regular search (containing language) and oligo search (comprising language)

claims priority to 09/062,365 4/17/1998

#### thanks

Christopher Yaen Patent Examiner Art Unit 1642 CM1-Rm 8E18 Mail Box 8E12 703-305-3586

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#### STIC-Biotech/Ch mLib

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> **Point of Contact: Toby Port Technical Info. Specialist** CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: 4/24
Date Completed: 424
Searcher Prep/Review: 1/0
Clerical:
Online time: //

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)	•
STN:	
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Human amyloid beta Human amyloid prot			Alzheimer-b	e ant	pep	Beta-amyloid 1-42	Synthetic amyloid	Human tachykinin a	in'	A-beta-binding pep	Human beta-amyloid	Human amyloid beta	Human amyloidogeni	Human beta amyloid	Full length beta-a	Beta-amyloid pepti	Neurotoxic beta-am	Beta A4 peptide.	Alzheimer amyloid	Beta/A4-amyloid pe	(1-	Sequence of A99 (b		$\alpha$	Beta-amyloid (1-41	Amyloid beta-prote			Ω	Partial sequence o	4	Synthetic amyloid

## ALIGNMENTS

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RESULT
Disclosure; Page 34; 51pp; English.
                 Detecting Alzheimer's disease using beta-amyloid peptide - includes quantitating amyloid deposition onto tissue samples, using screen agents as therapeutic agents
                                                                      Maggio JE, Mantyh PW;
                                                                                                                                                                      WO9304194-A.
                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                        Alzheimer's
                                                                                                                                                                                                                         Beta-amyloid peptide
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                                                     WPI; 1993-094020/11.
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                                                                                      (HARD ) HARVARD COLLEGE: (MINU ) UNIV MINNESOTA.
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RESULT
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05 | FEB-1993;
16 | NOV-1993;
28 | DEC-1993;
                                                                                                Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's
                                                                                                                                                                                            Antibodies recognising specific parts of beta-amyloid used for diagnosis of diseases implicating beta-amyloi Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                Amyloid precursor anti-beta-amyloid
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                                                                      Sequence
                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                          Kitada
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                    Conservative
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antibody; diagnosis.
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Query Match Best Local Matches

Local

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Score 40; DB 18; Pred. No. 5.8e-36; Mismatches 0;

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                                      CC A novel method has been developed of assaying for soluble amyloid CC precursor protein (sAPP). The method uses an antibody against amyloid CC beta-protein (A beta; produced from sAPP) or sAPP. The present sequence CC represents amino acids 1 to 40 of amyloid beta-protein. sAPP can be CC assayed accurately, and when including a monoclonal antibody recognising the N-terminus of A beta and a monoclonal antibody recognising sAPP, the CC assay can be used to diagnose Alzheimer's disease. Senior plaque CC observed in the brain of Alzheimer's patients is primarily composed of CC A beta, which is generated from sAPP, Simple and accurate assay of sAPP cis possible. The antibody (preferably monoclonal) preferably has an CC antigen recognition site which is an amino acid sequence common to CC A beta and sAPP, or specific to sAPP. The sAPP assayed for preferably CC solubilised through cleavage of the A beta between positions 16 (lysine) CC and 17 (leucine) from the amino acid terminus. The preferred method CC comprises immobilising one antibody (especially generated by (2)) on to CC antibody, reacting another, labelling, antibody with the assay substance cCC and detecting the activity of the labelling substance bound to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amyloid
amyloid
                                                                                                                                                                                                                                                                                                                                                                                         Assay for soluble amyloid precursor protein useful to diagnose Alzheimer's disease - uses antibodies against amyloid beta-protein, also new hybridoma producing antibodies
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Sequence
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precursor protein; soluble; APP;
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Peptides AAW23335-36 are portions of the the amyloid beta peptide, which CC is the principal component of extracellular deposits in Alzheimer's CC disease. It has been shown to promote nuerite outgrowth, generate CC reactive oxygen intermediates, induce cellular oxidant stress, lead to cellular oxidant stress, lead to competitive oxygen intermediates, induce cellular oxidant stress, lead to competitive oxygen intermediates, induce cellular oxidant stress, lead to cellular oxidate, which comprises annote is used in a pharmaceutical composition. The present cellular areceptor for advanced glycosylation of an amyloid beta peptide with a receptor for advanced glycosylation on the surface of a cell comprises contacting the cell with e.g. present peptide. Depending on the type of cell, inhibiting the interaction between the amyloid beta peptide and the cell withing the interaction between the amyloid beta peptide and the cepture for advanced glycosylation can be used for inhibiting cell beta peptide into a fibril, inhibiting extracellular assembly of amyloid beta peptide into a fibril, inhibiting aggregation of amyloid beta peptide into a fibril, inhibiting aggregation of amyloid beta peptide into a fibril, inhibiting aggregation of microglial cells by amyloid beta peptide. The methods can be used for treating e.g. cuberosis, neuronal cytotoxicity, Down's syndrome, dementia cassociated with head trauma, amyotrophic lateral sclerosis, multiple
Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting damage to cells in e.g. Alzheimer's disease - usi agent which inhibits interaction of an amyloid-beta peptide receptor for advanced glycosylation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amyloid beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23335 standard; peptide; 40
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amyloid beta peptide; extracellular deposit; Alzheimer's nuerite outgrowth; microglial activation; neuronal cell o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amyloid beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor for advanced glycosylation end product;
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Similarity 100
10; Conservative
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Score 40; DB Pred. No. 5.8 0; Mismatches
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5.8e-36;
hes 0;
                                     DB 18;
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                                  Length 40;
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DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

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RESULT
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                                                                                                                                                         Matches
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                          The present sequence was used in the development of a novel in vitro screening assay for agents capable of affecting the deposition of beta-amyloid peptide (BAP) on tissue. The method comprises contacting a silk sample with labelled BAP, optionally in the presence of a test agent, detecting the amount of label bound to the silk and assessing the effect of the agent on the deposition of BAP. Agents that inhibit binding of BAP to silk are potentially useful for treating amyloidosis diseases, especially Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening assay; beta-amyloid peptide; treatment; amyloidosis disease; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW47226 standard; peptide;
       Beta-amyloid protein
                           01-DEC-1999
                                                                  AAY39339
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                          New in vitro screening assay for Alzheimer's disease drugs -
comprises assessing binding of labelled beta-amyloid peptide
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-168404/15
                                                                                                                                                                                                                                                                                                                                                                                                            Maggio JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1994;
13-AUG-1991;
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                                                                                                                                                                   Local Similarity
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                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                HARVARD COLLEGE.
UNIV MINNESOTA.
                                                                standard; protein; 40
                                                                                                                                                                                                          40
                          (first entry)
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                                                                                                                                                         Conservative
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91US-0744767
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Pred. No.
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                                                                                                                                                         Mismatches
                                                                                                                                                                  5.8e-36;
                                                                                                                                                                            DB 19;
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RESULT
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XX AAY3
AC AAY3
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XX Bet
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's disease is characterised by the accumulation of a 39-43 amino acid peptide termed the beta-amyloid peptide in the form of extracellular amyloid plaques and as amyloid in the walls of cerebral blood vessels. The invention relates to methods for the formation of congophilic maltese-cross spherical amyloid plaques, which are characteristic of Alzheimer's disease. The amyloid plaques are formed by co-incubation of this beta-amyloid protein with sulphated macromolecules. The methods can be jused to study the formation of amyloid plaques and to identify anti-plaque therapeutics. They can be used for diseases such as Alzheimer's disease, Cretzfeidt-Jakob disease, Gerstmann-Straussler and the state of the sease of the sease
                                                                                                                                                                                                                                        Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling; long-standing inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru; carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPH;
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congophilic maltese-cross spherical amyloid plaque;
Creutzfeldt-Jacob disease; Gertsmann-Straussler syndrome
                                                                                                                                          subacute spongiform
                                                                                                                                                                            endocrine tumour; medullary carcinoma; Down's syndrome;
Creutzfeldt-Jakob disease; Gerstmann Strausiler Syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
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                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY39804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY39804 standard;
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les 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                          encephalopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta/A4 amyloid (1-40).
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                                                                                                                                          therapy
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5.8e-36;
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                                                                                                                                                                                                                        Human amyloid beta-A4 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiolucency in the wrist and hip, endocrine tumours, medullary of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (including B-cell type malignancies), Familial Mediterranean Fever, multiple myeloma, plasma cell dyscrasias, long-term haemodialysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a method for treating or preventing a form of amyloldosis, including Alzheimer's disease using this sequence. The compositions may be useful for treating or preventing the amyloldosis associated with long-standing inflammation, various forms of mallgnammation, various forms of mallgnammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a fragment of the beta-amyloid protein. The invention relates to a method for treating or preventing a form of
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23-SEP-1992;
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           WPI; 1999-403957/34.
                                                                            17-JUL-1996;
                                                                                                                       06-JUL-1999
                                                                                                                                                                                        Amyloid protein;
therapeutic drug
                                                                                                                                                                                                                                               26-AUG-1999
                                                                                                                                                                                                                                                                     AAY25135
                                                                                                                                                                                                                                                                                          AAY25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Creutzfeldt-Jakob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides of
                                                                                                 17-JUL-1996;
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tunnel
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                                                       HOECHST
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                                Paul JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subacute
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                                                                                                                                                                                        drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-8 amino acids useful for treating or
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                            96US-0682245
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92US-0950417
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                                                       MARION ROUSSEL
                                                                                                                                                                                        beta-A4 peptide; aggregation;
; brain; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joint swelling, multiple spontaneous
                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spongiform encephalopathies.
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                                 Riedel NG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83pp;
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                                                                                                                                                                                                   screening; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
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Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for the determination of the degree of aggregation of an amyloid beta A4 peptide (I) in solution. Determination comprises: (a) incubating a sample of unaggregated (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated (I); (b) measuring the amount of (II) bound to (I) to obtain a value (i); (c) repeating steps (a) and (b) with a second sample at a different time to obtain a second value (ii); and (d) determining the difference between (i) and (ii) which is inversely related to the degree of aggregation of (I). This method may be applied to a screen for compounds that inhibit aggregation of (I). These inhibitors may be used as therapeutic drugs to inhibit the formation of these aggregates in the brains of patients suffering from Alphaimer's disease.
and can be used in the method of the invention. The method is for inducing amyloid plaque deposition in a mammal by infusing into the brain an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque deposition has been induced are models of human Alzheimer's disease (AD) and are used to screen for agents (A) that inhibit: (a) deposition of amyloid plaque; and (b) An-associated disruptions to sleep and circadian activity. They may also be used to study the ethology of AD. Compared
                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MIRI-) MIRIAM HOSPITAL LIFESPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induction;
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                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                 ng amyloid plaque deposition against Alzheimer's disease
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                                                                                                                                                     represents a fragment of the human beta-amyloid ad in the method of the invention. The method is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human;
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                                                                                                                                                                                                                               43pp; English.
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ian activity; circadian rhythm disturbance
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RESULT
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                                                                                                                                                                                                   This sequence corresponds to an aggregating amyloid-beta peptide which can be covalently labelled with a fluorescent group. The detection or monitoring of an amyloid aggregate in a sample can be used to diagnose or detect a predisposition to Alzheimer's disease. The screening assay can be used to identify compounds for the treatment or amelioration of Alzheimer's disease or its symptoms. The fluorescent derivatives of the stream of the screening assay can be used to identify compounds for the treatment or amelioration of Alzheimer's disease or its symptoms. The fluorescent derivatives of the screening assay to the stream of the screening assay to the stream of the screening assay to the screening assay 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pH (I) is soluble enough for delivery by continuous infusion with fective delivery to brain tissue. The control peptide causes few, if any, plaques and does not stimulate an immune response. Most (I)-treated animals develop AD-type pathology (contrast transgenic models of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease),
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                                                                                                               Sequence
                                                                                                                                                                              Alzheimer's disease or its symptoms. amyloid-beta peptide are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-190112/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 21; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
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                100.0%;
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Pred. No.
                    Score 40;
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; DB 20;
. 5.8e-36;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       peptides
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                                                                                                                                                                                other aspects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
                                                40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                of.
                                                                                                                                                                                                                                             assays
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AAW81473
ID AAW8
XX AAW
AC AAW
DT 28-X
XX Syn
DE Syn
XX Amy
KW resi
                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                      This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzhaimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inharited congophilic angiopathy with cerebral haemorrhage. ANW2655-W92731 are tachykinin agonists derived from human had a control of the syndromes of hereditary cerebral haemorrhage.
          Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition; research; neurotoxicity; free-radical; glutamine synthetase.
                                                  Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
                                                                                28-JAN-1999
                                                                                                          AAW81473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1b; Column 41-42; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1991;
27-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5876948-A
                                                                                                                                 AAW81473 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachykinin agonist; beta-amyloid; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW92723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW92723 standard; peptide;
                                                                                                                                                                                                                                                                                                                                               beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                1999-189630/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tachykinin agonist beta-amyloid peptide
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0737371.
90US-0559173.
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                                                                                                                                 peptide;
                                                                             entry)
                                                                                                                                                                                                                                                                100.0%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                               fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Down's
                                                                                                                                   40
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome; amyloidosis;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-inherited congophilic angiopathy
                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                .8e-36;
                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurotoxin;
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment #69
                                                                                                                                                                                                                                                                            Length 40;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment;
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                    Gaps
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peptides. The invention provides a process for treating a synthetic Abbta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethy sulphoxide, morpholinopropanesulphonic acid, dimethylfornamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in te to determine free-radical generating capacity and glutamine synthetase
Sequence
                                                                                                                                                                                                                             Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic
                                                                                                                                                                                                                                                                                  Claim 5;
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-034120/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5840838-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                         Aksenov M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          (KENT ) UNIV KENTUCKY RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-FEB-1996;
                                                                                                                                                                                                                                                                                                                 for treating synthetic amyloid beta peptides - treatment, useful for studying neurotoxicity
                                                                                                                                                                                                                                                                                Columns 11-12; 14pp; English
 40
                                                                                                                                                                                                                                                                                                                                                                                                       Butterfield DA,
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                                                                                                                                                                                                                                                                                                                                                                                                       Carney JM,
                                                                                                                                                                                                                                                                                                                                                                                                         Hensley
                                                                                                                                                                                                                                                                                                                                  by organic
                                                                                                                                                                                            dimethyl
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                             Matches
                                 Query Match
Best Local Similarity
Conservative
                                   100.0%;
                            0;
                           Score 40; DB 20;
Pred. No. 5.8e-36;
; Mismatches 0;
 40
             40
                                         Length 40
                             Indels
                            0
                            Gaps
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AAE05483
                                            AAE05483 standard; peptide; 40
                                     (first entry)
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Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive; neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension; age-related cognitive function loss; senile dementia; Wilson's disease; Parkinson's disease; amylotrophic lateral sclerosis; cerebroprotective; cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia; Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma; Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease; myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke; Gilles de la Tourette's syndrome; nootropic; chronic seizure disorder; brain trauma; spinal cord trauma; acquired immunodeficiency syndrome; AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological; autonomic function disorder; Freidrich's ataxia; schizophrenia; therapy; vasotropic; neuroprotective; anti-HIV; human immunodeficiency virus; Human peptide antigen comprising beta amyloid (Abeta) 40.

epilepsy; neuroleptic;

immunostimulant

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RESULT 1
AAB84426
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear palsy, Guam disease, Lewy body dementia, prion diseases, spongiform encephalopathies, Creutzfeldt-Jakob disease, polyglutamine diseases, Huntington's disease, myottonic dystrophy, Freidrich's ataxia, ataxia, Gilles de la Tourette's syndrome, seizure disorders, epilepsy, chronic seizure disorder, stroke, brain trauma, spinal cord trauma, acquired immunodeficiency syndrome (AIDS) dementia, alcoholism, autism, retinal ischaemia, glaucoma, autonomic function disorder, hypertension, neuropsychiatric disorder, schizophrenia or schizoaffective disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders e.g. Alzheimer's disease, age-related loss of cognitive function, senile dementia, Parkinson's disease, amylotrophic lateral sclerosis, Wilson's disease, cerebral palsy, progressive supranuclea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to pharmaceutical compositions comprising complexes of heat shock proteins (has) in association with antigenic molecules for use in treatment and prevention of neurodegenerative disorders and diseases. The complexes of hsp and antigenic peptides are used as vaccines for the treatment or prevention of neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat shock protein and antigenic molecule complexes, useful for the prevention and treatment of neurodegenerative disorders e.g. senile dementia, Alzheimer's disease and epilepsy -
                             08-DEC-2000; 2000WO-US33203
                                                                                                                                                                                                                                                                                                                                                                 Partial sequence of a human beta-amyloid precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB84426 standard; peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and for eliciting an immune response. The present s peptide antigen comprising beta amyloid (Abeta) 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200152890-A1
                                                                                          14-JUN-2001
                                                                                                                                                  WO200142306-A2
                                                                                                                                                                                                                                                                                                             Beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0489216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; l Similarity 100.0%; 40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                       precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                       protein; APP; chimeric peptide; B cell epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DE Pred. No. 5.8 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 5.8e-36;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                            17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide cleavage product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a Northernic peptides contain a Northernic peptides contain a Northernic peptide cleavage product of a precursor or maturally occurring internal peptide cleavage product of a precursor or mature protein, as a free Northernic peptide to a Toell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betaAPP peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They also block the interaction of amyloid beta peptides with other molecules
                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 41; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to {\tt T} cell
                                                                                                                                                                                                                                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a partial sequence of a human beta-amyloid precursor protein (APP). The peptide is used to create
                                                                                                           17-MAY-2000; 2000WO-US13576
                                                                                                                                             23-NOV-2000
                                                                                                                                                                            WO200069900-A2
                                                                                                                                                                                                                                                           hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                            Amyloid beta-protein fragment peptide SEQ ID NO:956
                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                             AAB91780;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91780 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DAEFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          daefrhdsgyevhhqklvffaedvgsnkgaiiglmvggvv 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                            9908-0159783
                                                             99US-0134406.
99US-0153406.
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                                                                                                                                                                                                                                                           hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DE
Pred. No. 5.8
0; Mismatches
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. 5.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 40
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(CONJ-) CONJUCHEM INC

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Search completed: April 24,
Job time: 249 sec
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                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 40; DB 22; Best Local Similarity 100.0%; Pred. No. 5.8e-36; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112059/12.
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                                                                                                                                                                                                                                      7
                                                                                                                                                                     40 AA;
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                                2002, 09:21:50
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C;Species: Sus scrota domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chanev, M.O. Morrie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Cavia porcellus (guinea pry)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual,
Brain Res. Mol. Brain Res. 10, 299-305, 1991
Brain Res. Mol. Brain Res. 10, 299-307, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in A;Reference number: A60045; MUID:92017079
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JUNE 1975
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain Res. Mol. Brain Res. 10, 299-305, 1991 A; Title: Conservation of the sequence of the A; Reference number: A60045; MUID:92017079
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                                                                                                       A; Title: Conservation of the sequence of the Alzheimer's disease amyloid A; Reference number: A60045; MUID:92017079
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A; Residues: 1-57 <JOH>
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A; Residues: 1-57 <JOH>
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R; Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A;Reference number: A60045; MUID:92017079
A;Accession: A60045
                                                                                                                                                                       C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-57 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  A60045
Alzheimer's
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Best Local :
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6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV. 45
                                    1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain A; Figure: Conservation of the sequence of the A; Reference number: A60045; MUID:92017079
A.Arosseion. Profes A; Molecule type: mRNA A; Residues: 1-57 <JOH> R; Johnstone, A; Accession: B60045 Brain Res. Mol. C; Accession: B60045 C;Date: Alzheimer's Query Match Best Local Species: Matches Local Similarity es: Ursus maritimus (polar bear) 01-Dec-1992 #sequence\_revision 40; disease amyloid beta/A4 protein precursor -Jrsus maritimus (polar bear) E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P bl. Brain Res. 10, 299-305, 1991 100.0%; ilarity 100.0%; Conservative 0; Score 40; Pred. No. Mismatches 01-Dec-1992 #text\_change 13-Aug-1999 Alzheimer's disease amyloid peptide in 2.1e-35; DB Length Indels polar bear (fragment) 57; 0; Gaps proteinas 0;

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C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of tarbarence number: PQ0438; MUID:93075180
                                                                                                                                                                                                                       RESULT
PQ0438
                                                                                                                                          Alzheimer's disease amyloid A4 protein precursor C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995
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Copyright (c) 1993 - 2000 Compúgen Ltd
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219241 seqs,

Searched: 76174552 residues

Word size :

Total number of hits satisfying chosen parameters: 219241

Minimum pB seq length: 0
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Post-processing: Listing first 45 summaries PIR\_68:\* pir1:\*

pir2:\*

and is score No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

### SUMMARIES

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## ALIGNMENTS

R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra A;Reference number: PN0512; MUID:93290653

A;Accession: PN0512
A;Molecule type: prottein
A;Molecule type: prottein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; amyloid

Query Match Best Local Similarity "~+~hes 40; Conserv? 밁 Q 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40 100.0%; ilarity 100.0%; Conservative 0; 0; Score 40; DB 2; Pred. No. 1.6e-35; Mismatches 0; Length 42; Indels 0, Gaps 0

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment) C;Species: Ovis sp. (sheep) C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995 C;Accession: E60045 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res: 10, 299-305, 1991 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in A;Reference number: A60045; MUID:92017079

A;Molecule type: mRNA A;Residues: 1-57 <JOHD A;Cross-references: EMBL:x56130 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

δÃ 멍 Query Match Best Local S Matches 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40 9 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 45 Similarity 100.0%; ilarity 100.0%; Conservative 0 Score 40; DB 2; Pred. No. 2.1e-35 2.1e-35; thes 0; Length 57; Indels 0; Gaps

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Alzheimer's disease amyloid beta protein precursor [validated] - human N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibi N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular protein precursor splice form APP(770) C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000 C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I39453; I59562; A44 4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3 R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by A;Reference number: S02260; MUID:89128427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-695 < POD>
A; Cross-references: GB.M58727; NID:g342062;
C; Superfamily: Alzheimer's disease amyloid t
C; Keywords: alternative splicing
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A;Molecule type: DNA
A;Residues: 1-82 CDAV>
A;Cross-references: GB:M83558; GB:M83557
A;Cross-references: GB:M83558; GB:M83557
B;Johnstone, E.M.; Chaney, M.O.; Nortis, F.H.; Pascual, R;Johnstone, Mol. Brain Res. 10, 29-305, 1991
Brain Res. Mol. Brain Res. 10, 29-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal
C;Keywords: alternative splicing; Alzheimer's disease; amyloid;
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A; Cross-references: EMBL:X13466
A; Note: alternative splice form
R; Lemaire, H.G.
                                                                                                               A; Molecule type: DNA
A; Residues: 1-288, 'V', 365-770 <LEM1>
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A; Title: Homology of the amyloid beta protein
A; Reference number: A49795; MUID:91273117
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A; Residues: 12-68 < JOH>
                                                                                                                                                                                                 A; Accession: S02260
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Best Local S
Matches 40
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease amyloid
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R; Yoshikai, S.I.; Sasaki, H.; D
Gene 87, 257-263, 1990
A; Title: Genomic organization o
A; Reference number: 139451; MUI
A; Accession: 139452
A; Status: nucleic acid sequence
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A; Cross-references: EMBL:X13466; NID:g35598; PI
A; Note: alternative splice form APP(695)
R; La Fauci, G; Lahiri, D.K.; Salton, S.R.J.; R
Biochem. Biophys. Res. Commun. 159, 297-304, 19
A; Title: Characterization of the 5'-end region
A; Reference number: A32277; MUID:89165870
A; Accession: A32277
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 656-737 < LLEV>
A; Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A; Note: a mutation with 693-Gln is presented
R; Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB.M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Biochem. Biophys. Res. Commun. 170, 301-307, 1990 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene A;Reference number: A35486; MUID:90321244
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, N arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larsor Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A59020; MUID:91340168
A;Contents: annotation; erratum
A;Note: revised physical map for reference:
R;Levy, E.; Carman, M.D.; Fernandez-Madrid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:9178608; PIDN:AAB59501.1; PID:9178615
R;YOShikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Alzheimer's disease amyloid peptide is encoded by A;Reference number: A33260; MUID:89392030 A;Accession: A33260
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A; Reference number:
A; Accession: S05194
A; Molecule type: DNA
                                                                                                                                    A; Molecule type: DNA
A; Residues: 689-716, 'F', 718-737 < MUR>
                                                                                                                                                                                                                                           A; Title: A mutation in the amyloid precursor A; Reference number: I59562; MUID: 92022553
                                                                                                                                                                                                                                                                                                    R; Murrell, J.; Farlow, M.; Ghetti, Science 254, 97-99, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Mutation of the Alzheimer's disease A;Reference number: I39453; MUID:90260663 A;Accession: I39453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Levy, E.; Carman, M.D.; Fe
Science 248, 1124-1126, 1990
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A; Status: nucleic acid sequence
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A; Residues: 1-770 < YOS1>
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A; Residues: 672-710 < PRE1>
A; Note: 693-Gln was found
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A; Residues: 656-737 <JOH>
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A; Residues: 1-75 <LAF>
                                                                                                                                                                                             A; Status: translated
                                                                                                                                                                                                                    A; Accession: I59562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M33112; NID:g178613;
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H.; Doh-ura, K.; Furuya, H.;
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598; PIDN:CAA31830.1;
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familial Alzheimer disease kindreds

Larson,

E.

Heston,

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A; Reference number: A44017; MUID:9303537
A; Accession: A44017
A; Molecule type: DNA
A; Residues: 687-692; G; 694-718 < KAN1>
A; Residues: 687-718 < KAN2>
A; Note: sequence stracted from NCBI backbone (NCBIP:115374)
A; Accession: B44017
A; Molecule type: DNA
A; Experimental source: familial Alzhelmer disease family LIT
A; Molecule type: DNA
A; Experimental source: familial Alzhelmer disease family LIT
A; Molecule type: DNA
A; Experimental source: familial Alzhelmer disease family LIT
A; Molecule type: DNA
A; Experimental source: familial Alzhelmer disease family LIT
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: mRNA
A; References: GB; MID; MID: 87144572
A; Accession: A0134
A; Molecule type: mRNA
A; Residues: 1-288; V', 365-770 < KAN>
A; Residues: 1-288; V', 365-646; E', 648-770 < KON>
A; Residues: 1-288; V', 365-646; E', 648-770 < KON>
A; Residues: 1-288; V', 365-646; E', 648-770 < KON>
A; Residues: 1-288; V', 365-770 < KON>
A; Residues: 1-288; V', 365-77
                                                                                                                                                                                                                                      R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.;
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an A;Reference number: S00707; MUID:88122640
A;Recession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross:references: EMBL:X05982; NID:928817; PID:
A;Cross:references: EMBL:X05982; NID:928817; PID:
A;Cross:references: EMBC:X05982; NID:928817; PI
          A;Title: A new A4 amyloid mR
A;Reference number: S00925;
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-77
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A; Residues: 672-678 < DYR>
R; Tanzi; R.E.; McClatchey
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type: mRNA
: 1-344,'I',365-770
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Lemaire, H.G.; !
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                                                                                                          R;de Strooper, B.; van Leuven, F.; van den i
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor
A;Reference number: S19727; MUID:92096458
       A; Molecule type: mRNA
A; Residues: 1-210, 'G'
                                                                                                                                                                                                          A; Cross-references: GB:M18373;
A; Experimental source: brain
R; de Strooper, B.; van Leuven,
                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-695 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: A27485
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Blochem. Biophys. Res. Commun. 149, 665-671, 1987 A;Title: Complementary DNA for the mouse homolog ca;Reference number: A27485; MUID:88106489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; 149485
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212-220, 'S', 222-396, 'A', 398-402, 'T'

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NID:g191568;

PIDN:AAA37139

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A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573 A;NOte: the authors translated the codon GAA for residue 599 as Gly, ACC 18 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT A;Note: the cited Genbank accession number, J03594, is not in release 101. R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.;
                                                                                                                                                                                                                                                                                                                  R; Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988 A; Title: Molecular cloning of amyloid cDNA derived from A; Reference number: A31087; MUID:88124954 A; Accession: A31087
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 507-770 <ZAI>
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A; Residues: 606-770 <VIT3>
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A; Residues: 122-288, 'V', 365-770
A; Accession: C30320
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A;Status: not compared with conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: alternative splice form APP(770) R; Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, Brain Res. Mol. Brain Res. 4, 121-131, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X06981; NID:g2881
A;Experimental source: glioblastoma cell
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Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: not compared with
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A; Residues: 284-288, 'V', 365-770
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                    1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
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A:Experimental source: brain C:/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein F:625-648/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The beta-A4 amyloid precursor protein binding A;Reference number: $4625; MUID:94320627
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
A;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Mill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 18-37,'x', 39-40,'x', 42-44 <SCH>
A; Residues: 60 Apparan sulfate attachment
R; Hesse, L; Beher, D; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-695 <SHI>A;Cross references: EMBL:x07648; NID:g55616; PIDN:CAA30488.1; PID:g55617 R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G. Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate pr A;Reference number: A41245; MUID:88264430
A;Accession: A41245
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                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
                                                                                                                                                                                                                                                                                                           A; Reference number: A39820; A; Accession: A39820
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A; Residues: 1-695 <SH
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C;Keywords: alternative
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A; Residues: 1-19 < RES>
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A;Title: Positive and negative regulatory elements
A;Reference number: 149485; MUID:92209998
A;Accession: 149485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X59379
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Superfamily: Alzheimer's disease amyloid; Keywords: alternative splicing; amyloid;
    Query Match
Best Local Similarity
Matches 27; Conserv
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Position
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27; Conser
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       Conservative
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67.5%; Score 27; DB 100.0%; Pred. No. 9. tive 0; Mismatches
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transmembrane
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                          9.4e-21
                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                       beta-amyloid
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C;Accession: JH0773
R;Okado, H; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: de.
A;Reference number: JH0773; MUID:93129227
A;Accession: JH0773; MUID:93129227
A;Accession: JH0773; MUID:93129227
A;Accession: JH0773; MUID:93129227
A;Accession: JH0773
A;Residues: 1-747 <OKA>
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:9263151
A;Experimental source: larva
C;Superfamily: Alzheiner's disease amyloid beta protein; animal Kunitz-type C;Keywords: alternative splicing; amyloid beta protein homology <BPI>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease amyloid beta protein precursor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1
                                                                                                                                                                                                                                        3-oxoacyl-(acyl-carrier protein) reductase BH1842 [imported] - Bacillus halodurans c;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 C;Accession: B83880 C;Accession: B83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-33 < KOJ> C; Superfamily: Alzheimer
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S23094
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-247 <ST(
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R; Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
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                                                                                                                                                                          A; Title: Complete genome
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-amyloid protein precursor - rat
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17; Conserv
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                                                                                                                                             A83650;
                                                                                                                                         sequence of the alkaliphilic 50; MUID:20263314
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100.0%;
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A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05561.1; GSPDB:GN00 C;Genetics:
A;Genetics:
A;Gene: BH1842
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 KGAIIGL 34
Db 159 KGAIIGL 165

Search completed: April 24, 2002, 09:23:15

Job time: 244 sec
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Result
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Maximum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq
     Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-682-245A-2
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US-08-986-948-3
US-08-986-948-1
US-08-986-948-1
US-08-986-948-3
US-08-986-948-3
US-08-986-948-1
US-08-986-948-1
US-08-302-808-4
US-08-304-767A-2
US-08-304-767A-2
US-08-464-247A-19
US-08-464-247A-19
US-08-464-247A-19
US-08-464-247A-19
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US-08-304-5859A-19
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Query Matc Best Local Matches	RESULT 1 US-07-744-767a-: Sequence 1, A; Patent No. 54; GENERAL INFORMATION ITTLE OF II INUMBER OF I		228 229 330 331 331 331 331 331 331 331 341 341 341
ch 1 Similarity 40; Conservat	67A-1 1, Application 2, ANT: Mangpio, ANT: Mangpio, ANT: Mangpio, 2, OF INVENTION: 2, OF SEQUENCES 2,		40 1100.0 40 1100.0
100.0% 100.0%			44444444444444444444444444444444444444
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HOLLECULE TYPE:
US-08-235-400-2
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NAME: GAYLO, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: x-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                     Sequence 2, Application US/08476464A Patent No. 5707821
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                   APPLICANT: RYDEL, RUSSELL E. APPLICANT: DAPPEN, MICHAEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                COUNTRY: U.S.A.
ZIP: 94111-3834
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                     PPLICATION NUMBER:
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5. 5552426
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                                                                 CALIFORNIA
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Lilly Corporate Center/1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monn, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States
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                                                                                                                                                                    THERAPEUTIC INHIBITION OF PHOSPHOLIPASE A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; 100.0%; Pred. No.
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Patent No. 5721106
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Best Local Similarity
                                                                                TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino
STRANDEDNESS:
                                                                                                                                                                   NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                             STRANDEDNESS:
                                                             ENGTH:
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55458-1415
                                             amino acid
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                                                               40 amino acids
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Mantyh,
                                                                                                                    612-305-1228
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              not relevant
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                              not relevant
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Patrick W.
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                                                                                                                                                                                                                                                                               US/08/304,585
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Pred. No. 1.8e-34;
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US-08-302-808-3
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TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                             APPLICATION NUMBER: 344773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SUZUKI, NO. 57:
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
                                ANTI-SENSE:
                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 0190: FILING DATE: 05-FEB-1993 APPLICATION NUMBER: 2869 FILING DATE: 16-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15 CLASSIFICATION:
                                                                           TOPOLOGY:
                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                     40 amino acids
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                                                                           linear
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15-SEP-1994
                N-terminal
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Pred. No. 1.8e-34;
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Query Match

100.0%;

Score

40;

DB 1;

Length 40;

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-433-734-1
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                                                                                                                                                                                   Patent No.
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                                                                                                                                                                                                 Sequence 8,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.000101
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: HENSLEY, D. A.
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOY, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: 612-305-1220
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled
TITLE OF INVENTION: for Use i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
                                                                                                                                                                                                                                                                                         1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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5. 5837473
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Detecting Alzheimer's Disease
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US-07-737-371E-69
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: KIAUS, ETIC J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                            COMPUTER: IBM COmpatible OPERATING SYSTEM: Windows SOFTWARD
                                                                                                                                                  APPLICATION NUMBER: US/07/737,371E FILING DATE: 29-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                NAME: Freeman, John W
REGISTRATION NUMBER:
                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
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100.0%; P
ative 0;
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SCREENING METHODS TO IDENTIFY
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                00108/028002
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Pred. No.
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RESULT 9
US-08-682-245A-2
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                                                                                     ; MOLECULE TYPE: protein US-08-682-245A-2
   Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08682245A Patent No. 5919631
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:. HR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEWTZ, NELSEN L
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 17-JUL-19
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BA4 PEPTIDE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GOYAL APPLICANT: PAUL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                     TELLEFAX: J. TELLEFAX: 214320
                                                                                                                   TOPOLOGY:
                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                NAME: LENTZ, NELSEN L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 45215-6300
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TELEFAX: 617-542-8906
                                                                                                                                                                  LENGTH:
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                                                                                                                                                 amino acid
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                                                                                                                                                                    40 amino acids
   100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                513-948-7961 OR 4681
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PAUL, JOSEPH W
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0,
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                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1996
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Score 40; DB 2; I
Pred. No. 1.8e-34;
Mismatches 0;
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Pred. No. 1.8e-34;
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                              Matches
                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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APPLICATION NUMBER:
FILING DATE: 15-SEP-
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                               ANTI-SENSE:
                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 01013
APPLICATION NUMBER: 01903
APPLICATION NUMBER: 01903
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                           TELEFAX: 617-523-64
TELEX: 200291 STRE
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                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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RESULT 12
US-08-959-148-1
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                                                                                                                                                                                                                                                                                                                                        US-08-461-216-1
           GENERAL INFORMATION:
APPLICANT: Tate, Barbara A.
APPLICANT: Majocha, Ronald
APPLICANT: Mewton, Julie L.
TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL
FILE REFERENCE: 04930/022001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application Patent No. 5958883
                                                                                                        Sequence 1, Application Patent No. 6172277
                                                                                                                                                                                                                                                            Best Local Similarity Matches 40; Conserv
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CURRENT APPLICATION NUMBER: US/08/959,148
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MEDIUM TYPE: Diskette-5.25 inch,

COMPUTER: IBM PC/386 Compatible

COMPUTER: MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: September 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE: October
APPLICATION NUMBER:
FILING DATE: Septemk
                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
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                                                                                                                                                                                              ADDRESSEE:
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ilarity 100.0%;
Conservative 0
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{SYMBOL
FIGURES
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                                                                                                                      US/08959148
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er 23, 1992
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07/950,417
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1e, Suite 2800
                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                        Score 40; DB 2;
Pred. No. 1.8e-34;
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NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1

LENGTH:

40

CURRENT FILING DATE: 1997-10-28

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-959-148-1
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GENERAL INFORMATION:
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                                         Query Match
Best Local
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                           Matches
                                                                                                                                                                                                                                                                            TELEFAX: (612) 332-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                 MOLECULE TYPE: I
FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acid residues
                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (612) 332-5300
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                         FEATURE:
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                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Northgate OPERATING SYSTEM: DC SOFTWARE: WORDPERFEC
                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                           NAME: Kowalchyk, Alan W. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EILING DATE: 199208
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                                       Loca 1
                                                                                                                  LOCATION:
                                                                                                                                                                                                                        TOPOLOGY: Linear
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1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVV 40
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                                                                                                                                                                                                                                                                                       (612) 332-9081
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                                                                                                   Represents isolated internal sequence of 40 amino acid residues from the 'amyloid peptide precursor
                                                                                                                                                          Internal fragment of the
                                                                                                                                          amyloid peptide precursor
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                                                                                                                                                                             Peptide
Internal Fragment
Synthetically Derived
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Labelled -Amyloid Peptide
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                          100.0%; ; 100.0%; ; tive 0;
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                        Score 40; DB Pred. No. 1.8

D; Mismatches
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                                       1.8e-34;
                                                     DB 5;
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                                                        Matches
                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SUZUKI, NO.
APPLICANT: ODAKA, Asano
APPLICANT: KITADA
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 41 amino acid:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 28698:
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 33477:
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: LONGING BOSTON
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APPLICATION NUMBER: 01013
APPLICATION NUMBER: 01013
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                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 15-SEP-1994
                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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               1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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                                                      Score 40; DB 1;
Pred. No. 1.9e-34;
; Mismatches 0;
                                                                                   Length 41,
                                                        Indels
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Search completed: April 24, 2002, 09:22:29 Job time: 248 sec
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                                                                                                                                                             Query Match
Best Local Similarity
Tatches 40; Conserve
                                                                                                        Вþ
                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-682-245A-3
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                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 513-540
TELEX: 214320
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FENGTH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08682245A Patent No. 5919631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUI-1996
CLASSIFICATION: 435
CRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPAX: 513-948-7369
TELEPAX: 513-948-7361 OR 4681
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ZIP: 45215-6300
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: HOECHST MARION ROUSSEL, INC.
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BA4 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2110 E. C
CITY: CINCINNATI
STATE: OHIO
                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                  100.0%; ilarity 100.0%; Conservative
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OM protein - protein search, using sw model
                                                             Run on:
April 24, 2002, 09:20:47; Search time 21.46 Seconds (without alignments) 68.341 Million cell updates/sec
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Title: Perfect score:

Sequence: US-09-689-469-3
40
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Ouery Match 100.0%; Score 40; DB 1; I Best Local Similarity 100.0%; Pred. No. 1.2e-34; Matches 40; Conservative 0; Mismatches 0;

Length 57; Indels

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1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

6 15.0 322 1 PUR_HUMAN 6 15.0 327 1 POLG_PVYCH 6 15.0 327 1 COAT_PEMY 6 15.0 330 1 COAT_PEMY 6 15.0 389 1 IC.11_TR.HA 6 15.0 389 1 CPSD_STRAG 6 15.0 389 1 CPSD_STRAG 6 15.0 391 1 CPSD_STRAG 6 15.0 402 1 AAT_STRYG 6 15.0 402 1 GSPE_PSEAE 6 15.0 428 1 CPXL_PSESE 6 15.0 429 1 AROA_CORGL 6 15.0 429 1 AROA_CORGL 6 15.0 442 1 CEMI_YEAST	15.0 327 15.0 327 15.0 339 15.0 339 15.0 387 15.0 397 15.0 428 15.0 428 15.0 428 15.0 428 15.0 428 15.0 428 15.0 4429 15.0 4429 16.0 4429 17.0 442
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	1 POIG_PVYCH 200577 1 POIG_PVYCH 201294 1 COAT_PEMY P01793 1 IC11_TRIHA P17993 1 IC11_TRIHA P30014 1 CTRB_NEIMB P32014 1 CPSD_STRAG Q04664 1 AAT_STRVG Q04664 1 AAT_STRVG Q060013 1 GSPF_PSEAE Q050513 1 CPXL_PSESP P33006 1 AROA_CORGL P33016 1 AROA_CORGL P39525 1 AROA_MYCTU P22487
1 PUR_HUMAN 1 POLG_PWYCH 1 COAT_PEMY 1 ICI1_TRIHA 1 CTRB_NEIMB 1 CFSD_STRAG 1 CAT_STRVG 1 AAT_STRVG 1 GSPF_PSEAE 1 CPXL_PSESP 1 CPXL_PSESP 1 AROA_CORGL 1 CEM1_YEAST 1 AROA_MYCTU	00057 P21294 P07993 P34055 P3206604 Q04614 Q060013 Q00513 Q00513 P33006 P39525 P22487
PUR_HUMAN POLG_PVYCH COAT_PEMY IC11_TR.HA CTRB_NEIMB CPSD_STRNG AAT_STRNG GSPF_PSEAE CPXL_PSESP AROA_CORGL CEMI_YEAST AROA_MYCTU	00057 P21294 P07993 P34055 P3206604 Q04614 Q060013 Q00513 Q00513 P33006 P39525 P22487

# ALIGNMENTS

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EMBL; X56127; CAA39592.1;  HSSP; P05067; 1AML. InterPro; IPRO01868; A4_APP. InterPro; IPRO01868; A4_EXTRA; PARTIAL. PROSITE; PS00319; A4_EXTRA; PARTIAL. PROSITE; PS00320; A4_EXTRA; PARTIAL. Glycoprotein; Amyloid; Neurone; Transmembrane. NON_TER 1 1 CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL). DOMAIN <1 33 EXTRACELLULAR (POTENTIAL). TRANSMEM 34 57 POTENTIAL. NON_TER 57 57 POTENTIAL.		ב מיני בייני

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PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transm
NON_TER
1 1 BETA-AMYL
CHAIN 6 48 BETA-AMYL
DOMAIN <1 33 EXTRACELL
TRANSMEM 34 57 POTENTIAL
NON_TER 57 57
                       01-NOV-1997
01-NOV-1997
30-MAY-2000
ALZHEIMER'S
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Q29149;
Q1-NOV-1997
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INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIL INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIL
                                                                                                         028280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROFEIN HOMOLOG
    PROTEIN (BETA-APP)
                                                                                                                               A4_CANFA
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SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
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                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as an email to licenseelsb-sib.ch).
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                                                                                                                               STANDARD;
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                                  35, Created)
35, Last sequence up
39, Last annotation
    (A-BETA)] (FRAGMENT).
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                       AMYLOID A4 PROTEIN HOMOLOG
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POTENTIAL.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                    84209D88EBA82DFA CRC64;
                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                              update)
                                           update)
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                       [CONTAINS:
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Q28748;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                   PROILE... (APP. Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Tannmorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

Brain Res. Mol. Brain Res. 10:299-305(1991).

-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEINTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PATHWAY THROUGH THE GTP-BINDING
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                              MEDLINE-92017079; PubMed-1656157;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.,
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00319; A4_EXTRA; PARTIAL. PROSITE; PS00320; A4_INTRA; PARTIAL. Glycoprotein; Amyloid; Neurone; Tran
                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                        SEQUENCE FROM N.A.
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NON_TER
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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Mammalia; Eutheria;
Bovidae; Caprinae; C
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Q28757;
           between
the Euro
                                                                                                   MEDLINE=2017079; PubMed=1656157;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little "Conservation of the sequence of the Alzheimer's disease amyleptide in dog, polar bear and five other mammals by cross-sp polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).

-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING P
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30-MAY-2000 (Rel. 35
ALZHEIMER'S DISEASE
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PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
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FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
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SUBCELLULAR LOCATION: TYPE
SIMILARITY: BELONGS TO THE
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           SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Brain Res. Mol. Brain Res. 10:299-305(1991).
-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
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PROSITE; PS00319; A4_EXTRA; PARTIAL. PROSITE; PS00320; A4_INTRA; PARTIAL. Glycoprotein; Amyloid; Neurone; Tran
                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
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                                                                         EMBL; X56124; CAA39589.1; -. EMBL; X56126; CAA39591.1; -. HSSP; P05067; 1AML. InterPro; IPR001868; A4_APP.
                                                                                                                                                                                                    entities requires a or send an email to
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92017079; PubMed=1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  G(0) (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
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                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Neurone; Transmembrane.

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RESULT A4_SAIG ID_SAIG ID_SAIG
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Best Local Similarity
Matches 40; Conser
  PROSITE;
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TRANSMEM
DOMAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy E., Amorin A., Example of gene in squirrel monkeys with Beta-amyloid angiopathy.", cerebral amyloid angiopathy.", Neurobiol. Aging 16:805-808(1995).

-I-- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO THE FUNCTIONS STONALING PATHWAY THROUGH THE GTP-BINDING.
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Q95241;
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a control of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatically the statement is not removed.
                                                                      SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
                                                                                                                PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver, and Kidney; MEDLINE-96108492; PubMed-8532114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE ANYLOID A4 PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                         entities requires
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                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SÜBÉCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTAL FOR ITS
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFI
RECOGNITION EXTENDS TO PETTIDE RESIDUES THAT ARE C-TERR
MPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDE PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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Pro; IPR002223; Kunitz_BPTI.
PF02177; A4_EXTRA; 1.
PF00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                         S81024; AAD14347.1;
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PS00319; A4_EXTRA; 1.
PS00320; A4_INTRA; 1.
PS00280; BPTI_KUNITZ_1;
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U 4 8 8 8 8 8
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Chordata; Craniata; Ver
Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                         license agreement
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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ene in squirrel monkeys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
ni; Cebidae;
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Cebinae; Saim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TERMINAL
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13-AUG-1987 (Rel. 05, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHELMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR
ALZHELMER'S DISEASE AMYLOID BETA-AMYLOID PROTEIN (F
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MEDLINE-87144572; PubMed-2881207;
MEDLINE-87144572; PubMed-2881207;
Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters
Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.
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                                             Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Unterbeck A., Beyreuther K., Mueller-Hill B., "The PreA4 (695) precursor protein of Alzheimer's is encoded by 16 exons.";
Nucleic Acids Res. 17:517-522(1989).
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                                                                                                                                       "A new A4 amyloid mRNA contains proteinase inhibitors.";
Nature 331:525-527(1988).
[3]
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Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller
Greenberg B., Davis K., Wallace W., Lieberburg I., 1
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Nature 325:733-736(1987).
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Tanzi R.E., McClatchey A.I.,
Gusella J.F., Neve R.L.;
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Pardridge W.M., Vinters H.V., Yang J., Eisenberg
Tourtellotte W.W., Huebner V., Shively J.E.;
"Amyloid angiopathy of Alzheimer's disease: amino
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MEDLINE-87231971; PubMed-3035574;
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MEDLINE=88122641; Pu
                   Johnson-Wood
Sinha S.;
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citz L.C., Schenk
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Kamarck M.E., Ramabhadran
Tamburini P.P.;
"Sequential NMR resonance
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MEDLINE=92031488; PubMed=1718421;
Heald S.L., Tilton R.F. Jr., Hamm
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disease amyloid protein precursor.";
Biochem. Biophys. Res. Commun. 167:716-721(1990)
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MEDLINE=91104913; PubMed=2125487;
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MEDLINE=93188965;
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                                                                                                                               STRAIN-CD-1; TISSUE-Placenta; MEDLINE-89345111; PubMed-2569710; Fukuchi K., Martin G.M., Deeb S.S.; "Sequence of the protease inhibitor domain precursor of Mus domesticus."; Nucleic Acids Res. 17:5396-5396(1989).
            "Positive and negative regulatory elements Alzheimer's disease amyloid precursor-encocene 112:189-195(1992).
                                                                         MEDLINE-92209998;
Izumi R., Yamada
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Mammalia; Eutheria;
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Best Local
            PIR; S00550; S00550.

PIR; S03607; S03607.

InterPro; IPR001868; A4_APP.

InterPro; IPR002223; Kunitz_BPTI.

Pfam; PF002177; A4_EXTRA; 1.

Pfam; PF00214; Kunitz_BPTI; 1.

PRINTS; PR00203; AWYLOIDA4.

PRINTS; PR00759; BASICPTASE.

PRINTS; PR00759; BASICPTASE.
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P08592;
                                                                                                                                                                                           EMBL;
PIR;
PIR;
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"The
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01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMO
                                                                                                                                                                                                                                    EMBL; X07648; CAA30488.1; -. EMBL; X14066; CAA32229.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=88312583;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 289-364 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seeburg P.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Alzheimer's disease amyloidogenic in rat brain suggests a role in cel 3MBO J. 7:1365-1370(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMYLOIDOGENIC GLYCOPROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g J., Mueller-Hill B.;
e sequence of the two extra exons in rat preA4.";
leic Acids Res. 17:2130-2130(1989).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION THE CLATHRIN-BETA, AND GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLICING.
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    SM00006;
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    A4_EXTRA;
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salbaum J.M.,
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thi; Muridae; Murinae; Rat
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RESULT 11
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PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00320; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
Glycoprotein; Amyloid; Neurone; Transl Alternative splicing; Serine protease SIGNAL 1 17

BY SIMIL
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01-MAR-1992
01-NOV-1997
20-AUG-2001
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SEQUENCE
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SEÓUENCE FROM N.A.
STRAIN-*[12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D Mau B., Shao Y.;
                                                                                     "Organization of genes encoding membrane coli ferrienterobactin permease."; Mol. Microbiol. 5:1405-1413(1991).
                                                                                                                                                                                   "Nucleotide sequence and genetic organization of enterobactin transport system: homology to other protein-dependent systems in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
                                                                                                                                                                      protein-dependent systems in Eschemol. Microbiol. 5:1415-1428(1991).
                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL MEMBRANE YBDA OR B0591.
                                                                                                                                                                                                                                                                                                                                                                                       YBDA
                                                                                                                      Chenault S.S.,
                                                                                                                               MEDLINE=92157867; PubMed=1787794;
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                      Shea C.M., McIntosh M.A.;
                                                                                                                                                                                                                                 MEDLINE=92157868; PubMed=1838574;
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Last annotation
PROTEIN P43.
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CLAPHRIN-BINDING (BY SIMILARITY)
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BY LINKED (GLCNAC...) (POTENTIA
N-LINKED (GLCNAC...) (POTENTIA
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CYTOPLASMIC (PEQUIVALENT OF
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Pred. No.
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BY SIMILARITY.
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DF BETA-AMYLOID
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TRANSMEM 22 42
TRANSMEM 56 76
TRANSMEM 96 116
TRANSMEM 119 139
TRANSMEM 157 177
TRANSMEM 179 199
TRANSMEM 219 239
TRANSMEM 257 277
TRANSMEM 257 277
TRANSMEM 357 377
TRANSMEM 357 377
TRANSMEM 379 399
SUBMITTED (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: REQUIRED, PROBABLY INDIRECTLY, FOR THE HYDROXYLATION
2-OCTAPRENYL-PHENOL TO 2-OCTAPRENYL-6-HYDROXY-PHENOL, THE FOURTH
STEP IN UBIQUINONE BIOSYNTHESIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., L. Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Q9L6M4;
Q9L6M4;
Q9L6M4;
Q10-AUG-2001 (Rel. 40, Created)
Q10-AUG-2001 (Rel. 40, Last sequence update)
Q10-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE UBIQUINONE BIOSYNTHESIS PROTEIN UBIB
UBIB OR AARF OR STMD1.17.
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                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                  SALTY
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                                                                                                                SEQUENCE FROM N.A
                                                                                                                                            NCBI_TaxID=602;
                                                                                                                                                            Salmonella.
                                                                                                                                                                                            Salmonella typhimurium
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S16295; S16295.
S16306; S16306.
S14850; S14850.
Gene; EG11104; ybdA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                            GLMVGGV
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X59402; CAA42044.1; -.
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42
POTENTIAL.
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01-JUN-1994
01-JUN-1994
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PIR; S10640; S
SEQUENCE 64
PROF_ENTHI STANDARD;
P49230;
01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90294291; PubMed=2359120; Puyet A., Greenberg B., Lacks S.A.; Puyet A., Greenberg B., Lacks S.A.; "Genetic and structural characterization of endA. A membrane-bound nuclease required for transformation of Streptococcus pneumoniae."; J. Mol. Biol. 213:727-738(1990).
                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
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NCE 64 AA; 7037 MW;
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                                                                                                                                           Similarity 6; Conserv
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546 AA; 63238 MW;
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(Rel.
(Rel.
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Pred. No
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01-FEB-1996 (Rel. 15-DEC-1998 (Rel.

33, 37,

Last sequence update)
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NU6M_CEPCO
ID NU6M_C
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Best Local S
Matches 6
SEQUENCE FROM N.A.

MEDLINE-94363783; PubMed-8082208;

Moum T., Willassen N.P., Johansen

"Intragenic rearrangements in the
subunit 6 gene of vertebrates.";

Curr. Genet. 25:554-557(1994).
                                                                                                                                                                                                                                                                        NU6M_CEPCO
P43197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00235; profilin; 1.
SMART; SM00392; PROF; 1.
PROSITE; PS00414; PROFILIN; 1.
Actin-binding; Cytoskeleton.
SEQUENCE 130 AA; 13237 MW;
                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).
MTND6 OR ND6 OR NADH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The basic isoform of profilin in pathogenic Entamoeba histolytica.cDNA cloning, heterologous expression, and actin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
                                                                                                                                                              Mitochondrion.
                                                                                                                                                                           Cepphus columba (Pigeon guillemot).
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                                                                                                             Archosauria; Aves;
NCBI_TaxID=28696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002097; Profilin.
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20 GAIIGL 25
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mes 6; Conserv
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FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                      STANDARD;
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Erben H., Scheiner O., Wiedermann
                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; 50
100.0%; Pr
0;
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                      S.;
mitochondrial NADH dehydrogenase
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                                                                                                                                                    Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 173 AA; 17982 MW; AAAF84636E040DF8 CRC64;
                                                                                                                                                                                    Pfam; PF00499; oxidored_q3; 1
                                                                                                                                                                                                                     EMBL; X73918; CAA52123.1;
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98 LMVGGV 103
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                                                                   Conservative
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Search completed: April 24, Job time: 246 sec 2002, 09:24:53

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Result
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Perfect score:
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ALIGNMENTS

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#### AID DICTOR REPORTED TO THE REPORT OF THE THE REPORT OF THE P78438 Kamino K., Orr H.T., Payami H., Wijsman E.M., A Anderson L., O'dahl S., Nemens E., White J.A.; "Linkage and mutational analysis of familial Al kindreds for the APP gene region."; Am. J. Hum. Genet. 51:998-1014(1992). EMBL, M29270; AAA51768.1; JOINED. EMBL; M29269; AAA51768.1; JOINED. EMBL; M15532; AAA51768.1; JOINED. EMBL; M15532; AAA51768.1; -. EMBL; M15532; AAA5164.1; -. EMBL; M15532; AAA51768.1; JOINED. EMBL; M15532; AAA51768.1; -. EMBL; M15532; -. P78438 P78438; 01-MAY-1997 01-MAY-1997 01-MAR-2001 Biochem. SEQUENCE OF 19-48 FROM N.A. MEDLINE-87120329; PubMed=2949367; Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.; "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus."; Science 235:880-884(1987). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; "Alzheimer's disease amyloid peptide is encoded by similarity to soybean trypsin inhibitor."; Biochem. Biophys. Res. Commun. 163:1248-1255(1989). SEQUENCE FROM N.A. MEDLINE=89392030; PubMed=2675837; AMYLOID MEDLINE=93035397; PubMed=1415269; SEQUENCE OF 32-63 FROM N.A Little S.P.; Johnstone E.M., Chaney M.O., NCBI\_TaxID=9606; 1997 (TIEMBLIEL. 03, Last sequence update) 2001 (TIEMBLIEL. 16, Last annotation update) PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT). 7 (TrEMBLrel. 7 (TrEMBLrel. 1 (TrEMBLrel. PRELIMINARY; 03, 03, 16, Created) Moore Catarrhini; Hominidae; Craniata; Vertebrata; Euteleostomi; PRT; Wijsman E.M., R.E., 82 Ward AA Alzheimer disease Alonso M.E., Pulst S.M., K.E., two exons and shows Norris Homo F.H.,

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MEDIANNE-93236601; PubMed-8476439;
MEDIANNE-93236601; PubMed-8476439;
Denman R.B., Rosenzcwally R., Miller D.L.;
Denman R.B., Rosenzcwally R., Miller D.L.;
Passing of the effect(s) of familial Alzheimer disease
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   F534AA50E579230A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F534AA5B3EA9230A CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8DA9E42B813A070E CRC64;
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Pred. No.
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Best Local :
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                                                    Barnes N.Y., Ling L., Yoshikawa K., Milligan C.E.;
"Increased production of amyloid production (JAN-1998) to the EMBL/GEMBL; AR042098; AAC25052.1;
HSSP; P05067; 1BA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-93236601; PubMed-8476439;
MEDLINE-93236601; PubMed-8476439;
Denman R.B., Rosenzcwaig R., Miller D.L.;
Phasystem for studying the effect(s) of familial Alzheimer disease mutations on the processing of the betta-amyloid peptide precursor.";
mutations on the processing of the betta-amyloid peptide precursor.";
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01-NOV-1996;
01-NOV-1996;
01-MAR-2001;
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SEQUENCE
 PROSITE;
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Homo sapiens (Human).

""baryota; Metazoa; Chordata;
""heria; Primates;
                                                                                                                                                                                                                     Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                               01-NOV-1998
01-JUN-2001
                            InterPro; IPR001868; A4_APP
PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                          Archosauria;
                                                                                                                                                                                                                                                AMYLOID PRECURSOR PROTEIN (FRAGMENT).
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PS00319; A4_EXTRA; PS00320; A4_INTRA;
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el. 16, Last annotation update)
PRECURSOR (FRAGMENT).
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                                                                                                                                    Oppenheim R.W.
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Neurochem. Int. 0:0-0(2000).
EMBL; AFG30341; AAF12698.1; -.
HSSP; P05067; IBA4.
InterPro: IDDAA.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-JUN-2001
SEQUENCE FROM N.A.
TISSUE-BRAIN;
Beck M., Mueller D., Bigl V.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q60496;
Q60496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00203; AMYLOIDA4.
SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA;
PROSITE; PS00320; A4_INTRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001868; A4_APP.
Pfam; PF02177; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
Coulson E.J., Paliga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PVL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PVL1
                                                                                                                                                                                                          NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gallus (Chicken).
ota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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2000 (TrEMBLrel. 13, Last sequence update)
2001 (TrEMBLrel. 17, Last annotation update)
PROTEIN PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; a; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
60597
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ne amyloid p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                         Hystricognathi;
                                                                                                                                                                                                                                                                           Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OAB8BB851863A19D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FB53ECC2E66D4C92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695
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thes 0;
                                                                                                                                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                         Caviidae;
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                                                                                                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                    RESULT
Q9DGJ7
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Best Loc
Matches
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597
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O9DGJ8;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
Gallus gallus (Chicken).
                                                  01-MAR-2001 (TrEMBLrel. 16, Last sequence u 01-JUN-2001 (TrEMBLrel. 17, Last annotation BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
                                                                                                                                                                                                                                                                                                                                       PROSITE;
SEQUENCE
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                    Gallus gallus (Chicken).
                                                                  Q9DGJ7;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL; AF289218; AAG00593.1; InterPro; IPR001868; A4_APP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarasa M., Rodolosse A., "Cloning of full-length isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0203; AMYLOIDA4.
SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
SEQUENCE 695 AA; 78701 MW;
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001868; A4_APP. Pfam; PF02177; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X97631; CAA66230.1;
HSSP; P05067; 1BA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I
-!- SIMILARITY: TO OTHER SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local |
                                                                                                                                                                                                                                                               Match
Local Similarity
es 40; Conser
                                                                                                                                                                                                                                                                                                                                      n; PF02177; A4_EXTRA; 1.

NTS; PR00203; ANYLOIDA4.

RT; SM00006; A4_EXTRA; 1.

SITE; PS00319; A4_EXTRA; 1.

GENCE 695 AA; 78565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN \mathsf{G}(0) .
                                                                                                                                                                                                                     DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
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                                                                                                                                                                                                        DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 100
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROM N.A.
Rodolosse
                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chicken
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                                                                                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                             Score 40; DE
Pred. No. 1.5
0; Mismatches
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Pfam; PF00014; Kunitz_BPTI; 1.
Pfam; PF000203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
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Q9TUIO; PREMBLEEL 13,
01-MAY-2000 (TIEMBLIEL 13,
01-MAY-2001 (TIEMBLIEL 17,
01-UN-2001 (TIEMBLIEL 17,
                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                       PROSITE: PS00319; A4_EXTRA; 1.
PROSITE: PS00320; A4_INTRA; 1.
PROSITE: PS00280; BPTI_KUNITZ_1;
PROSITE: PS50279; BPTI_KUNITZ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimura A., Takahashi T.;
"Amyloid Precursor Protein 770.";
"Amyloid (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO PANCREATIC TRYPSIN INHIBITOR (KUNITZ)
EMBL; AB032550; BAA84580.1; -.
HSSP; P05067; IAAP.
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02177; A4_EXTRA; 1. Pfam; PF00014; Kunitz_BPTI; 1.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO PANCREATIC TRY EMBL; AF289219; AAG00594.1; InterPro; IPR001868; A4_APP. InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                     Serine protease inhibitor. SEQUENCE 770 AA; 86961
                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                              PRINTS; PR00203; AMYLOIDA4. PRINTS; PR00759; BASICPTASE.
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InterPro: IPR002223; Kunitz_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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SM00131; KU; 1.
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chicken beta-amyloid
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                                        Score 40; DE Pred. No. 1.7); Mismatches
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OR (KUNITZ) DOMAIN.
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Q13778;
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O9UC33; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence up
O1-MAR-2001 (TrEMBLE). 16, Last annotation
                                                                                                  MEDLINE-93024877; PubMed=1406936; Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.; Isolation and quantification of soluble Alzheimer's bet biological fluids."; Mature 359:325-327(1992).
HSSP, P05067; 1BA4.
HSSP, P05067; 1BA4.
SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization and chromosomal localization brain amyloid of Alzheimer's disease."; Science 235:877-880(1987).
EMBL; M15533; AAA35540.1; -.
HSSP; P05067; 1BA4.
Interpro; IPR001868; A4_APP.
PRINTS; PR00203; AMYLOIDA4.
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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SEQUENCE
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                                            th 82.5%; Similarity 100.0%; 33; Conservative
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Pred. No.
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Catarrhini; Hominidae;
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Pfam; PF00014; Kunitz_BPTI; 1.
PRANTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     073683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001868; A4_APP
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  691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPXY MOTIF. THIS INTERACTION APPEARS 1
PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY
SIMILARITY: CONTAINS 1 PROTEASE INHIB:
BPTI/KUNITZ FAMILY OF INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE CLATHEAU-BINDING SITE IS ESSENTIAL FOR ITS ASSOC
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTRACELLULAR SIGNALING PATHWAY THROUGH
YEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 721
                      YEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease
                                                                                                     Similarity
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                                                                             77.5%; illarity 100.0%; Conservative C
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733
323
769
327
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0320; A4_INTRA; 1.
0280; BPTL_KUNITZ_1; I
0279; BPTL_KUNITZ_2; 1
0279; BPTL_KUNITZ_2; 1
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711
732
780
382
772
378
361
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                                                                                                                                                                                         88238
                                                                                                                                                                                         WW;
                                                                           Score 31; DB; Pred. No. 7.10; Mismatches
                                                                                                                                                                                                                               POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BPTI/KUNITZ INHIBITOR.

CLATHRIN-BINDING (BY SIMII
BY SIMILARITY.

BY SIMILARITY.
                                                                               0;
                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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HOMOLOG.
                                                                                                                                                                                     60071BE94520191D
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
BETA-AMYLOID PEPTIDE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UCD1;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wisniewski T., Lalowski M., Levy E., "The amino acid sequence of neuritic Alzheimer's disease patient."; Ann. Neurol. 35:245-246(1994).
HSSP; PO5067; 1BA4.
SEQUENCE 30 AA; 3391 MW; FF4167AE
                                                                                                                                                                                                                                                          MEDLINE-94045685; PubMed-8229004; Vigo-Pelfrey C., Lee D., Keim P., "Characterization of beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAY-2000
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SEQUENCE 28
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                                                                                Similarity 27; Conser
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O (TrEMBLrel.
1 (TrEMBLrel.
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Primates;
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Catarrhini;
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Search completed: Job time: 249 sec

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Beta-amyloid prote
Human amyloid beta
Human beta-amyloid
Wild type aggregat
Human tachykinin a
                                                                                                                                                                          Description
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Human amyloid beta Human amyloid beta Sequence of A99 (b) Beta-amyloid (1-42 Beta-A4-amyloid pe Alzheimer amyloid Beta A4 peptide.  Neurotoxic beta-am Beta amyloid pepti Full length beta-a Human amyloid beta Human amyloid beta Human beta-amyloid A-beta-binding pep Mutant aggregating Human tachykinin a Synthetic amyloid Beta-amyloid 1-42 Amyloid-beta pepti Human peptide anti Human peptide anti Human peptide anti Human peptide anti Human myloid beta-prote Amyloid beta-prote Human amyloid beta-full beta human amyloid beta Human amyloid beta-prote Human amyloid beta Human amyloid prot	Synthetic amyloid Human peptide anti Partial sequence o Amyloid beta-prote Amyloid beta-prote Amyloid beta-prote Amyloid beta-prote Amyloid beta-prote Beta-amyloid (1-41

## ALIGNMENTS

RESULT AAR33191

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Alzheimer's disease; amyloid deposition; diagnosis; therapy.
                                                                                                                                                                                                                                          01-JUL-1993
                                                                                                                                                                                                                                                                            AAR33191 standard; peptide;
               using screen agents as therapeutic agents
                        Detecting Alzheimer's disease using beta-amyloid peptide includes quantitating amyloid deposition onto tissue sam
                                                   WPI; 1993-094020/11.
                                                                                                                13-AUG-1991;
                                                                                                                                                   04-MAR-1993.
                                                                                                                                                                     WO9304194-A
                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                       Beta-amyloid peptide
                                                                                                                                                                                                                                                            AAR33191;
                                                                     Maggio JE, Mantyh PW;
                                                                                     (HARD ) HARVARD COLLEGE. (MINU ) UNIV MINNESOTA.
                                                                                                                                 10-AUG-1992;
                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                 92WO-US06700.
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Disclosure; Page 34; 51pp; English

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Best Local
                                                                                                                                                                                                                                 Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amyloid precursor protein; APP; Alzheimer's disease; anti-beta-amyloid antibody; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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16-NOV-1993;
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Pred. No. 3.5e-24;
Mismatches 0;
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Pred. No. 3.5e-24;
Mismatches 0;
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Query Match Best Local Matches

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amyloid
                                                                                                                                                                                                                                                                                                                                                                                           precursor protein (sAPP). The method uses an antibody against amyloid beta-protein (A beta; produced from sAPP) or sAPP. The present sequence represents amino acids 1 to 40 of amyloid beta-protein. SAPP can be assayed accurately, and when including a monoclonal antibody recognising the N-terminus of A beta and a monoclonal antibody recognising sAPP, the assay can be used to diagnose Alzheimer's disease. Senfor plaque observed in the brain of Alzheimer's patients is primarily composed of
                                                                                                                                                                                            A beta , which is generated from sAPP. Simple and accurate assay of sAPP is possible. The antibody (preferably monoclonal) preferably has an antigen recognition site which is an amino acid sequence common to A beta and sAPP, or specific to sAPP. The sAPP assayed for preferably has part of the A beta sequence at its amino terminus and is preferably solubilised through cleavage of the A beta between positions 16 (lysine) and 17 (leucine) from the amino acid terminus. The preferred method
                                                                            comprises immobilising one antibody (especially generated by (2)) on an insoluble carrier, capturing a substance to be assayed on to this antibody, reacting another, labelling, antibody with the assay substand detecting the activity of the labelling substance bound to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assay for soluble amyloid precursor protein useful to diagnose Alzheimer's disease - uses antibodies against amyloid beta-protein, also new hybridoma producing antibodies
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel method has been developed of assaying for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2; 10pp; English.
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AAW23335
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Best Local :
                                          Matches
                                                                                                                                                                                                                                                                                      a receptor for advanced glycosylation end product and a carrier. A method for inhibiting interaction of amyloid beta peptide with a receptor for advanced glycosylation on the surface of a cell comprises contacting the cell with e.g. present peptide. Depending on the type of cell, inhibiting the interaction between the amyloid beta peptide and the receptor for advanced glycosylation can be used for inhibiting degeneration of a neuronal cell, inhibiting formation of an amyloid beta peptide into a cell, inhibiting extracellular assembly of amyloid beta peptide into a fibril, inhibiting aggregation of amyloid beta peptide on the surface of a cell, inhibiting infiltration of a microylial peptide on the surface of a cell, inhibiting infiltration of a microylial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is the principal component of extracellular deposits in Alzheimer's disease. It has been shown to promote nuerite outgrowth, generate reactive oxygen intermediates, induce cellular oxidant stress, lead to neuronal cytotoxcity, and promote microglial activation. The present peptide, which comprises amino acids 1-40 of the amyloid beta peptide, is used in a pharmaceutical composition. This composition comprises an agent capable of inhibiting interaction of an amyloid beta peptide with
                                                                                                                                                                                       cell into senile plaques, and inhibiting activation of microglial cells by amyloid beta peptide. The methods can be used for treating e.g. diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia associated with head trauma, amyotrophic lateral sclerosis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amyloid beta peptide; extracellular deposit; Alzheimer's disease; nuerite outgrowth; microglial activation; neuronal cell degeneration; receptor for advanced glycosylation end product; amyloid beta peptide fibril.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAW23335-36 are portions of the the amyloid beta peptide, which is the principal component of extracellular deposits in Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4;
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent which inhibits interaction of an amyloid-beta peptide with receptor for advanced glycosylation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9726913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amyloid beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1998
                                                          Local Similarity
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 10; 91pp; English
                                                                                                                                                                        or neuronal degeneration.
                                                                                                                                        40
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stern D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide 1 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0592070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US00857.
                                                          100.0%;
                                        0;
                                    Score 209; DB 18;
Pred. No. 3.5e-24;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibit damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells in Alzheimer's
                                                                         Length
                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitro screening assay for agents capable of affecting the deposition of beta-amyloid peptide (BAP) on tissue. The method comprises contacting a silk sample with labelled BAP, optionally in the presence of a test agent, detecting the amount of label bound to the silk and assessing the effect of the agent on the deposition of BAP. Agents that inhibit binding of BAP to silk are potentially useful for treating amyloidosis diseases, especially Alzheimer's disease.
                  Beta-amyloid protein
                                                                     01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence was used in the development of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New in vitro screening assay for Alzheimer's disease drugs - comprises assessing binding of labelled beta-amyloid peptide to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maggio JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening assay; beta-amyloid peptide; treatment; amyloidosis disease; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW47226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW47226 standard;
                                                                                                                                                                  AAY39339 standard; protein; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-1994;
13-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5721106-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-1998
                                                                                                                                                                                                                                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Columns 29-30; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mantyh PW;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0304585
91US-0744767
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 209; DB 19;
Pred. No. 3.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    affecting the method
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                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
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Best Local Similarity
Matches 40; Conser
                                                                    long standing inflammation; malignancy; Familial Mediterranean Fever multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; ku; carpal tunnel syndrome; multiple spontaneous fracture; radiolucency; endocrine tumour; medullary carcinoma; Down's Syndrome; scrapie; Creutzfeldt-Jakob disease; Gerstmann Strausiler Syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease is characterised by the accumulation of a 39-43 amino acid peptide termed the beta-amyloid peptide in the form of extracellular amyloid plaques and as amyloid in the walls of cerebral blood vessels. The invention relates to methods for the formation of congophilic maltese-cross spherical amyloid plaques, which are characteristic of Alzheimer's disease. The amyloid plaques are formed by co-incubation of this beta-amyloid protein with sulphated macromolecules. The methods come be used to study the formation of amyloid plaques and to identify anti-plaque therapeutics. They can be used for diseases such as Alzheimer's disease, Cretzfeldt-Jakob disease, Gerstmann-Straussler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Formation of amyloid plaques using amyloid protein and sulphated macromolecules, for, e.g. identification of agents for treating Alzheimer's disease \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castillo G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque; cerebral blood vessel; sulphated macromolecule; Kuru; congophilic maltese cross spherical amyloid plaque;
                             Homo sapiens
                                                          subacute spongitorm
                                                                                                                                                Beta-amyloid protein; Alzheimer's disease; amyloidosis;
                                                                                                                                                                               Beta-amyloid
                                                                                                                                                                                                            29-NOV-1999
                                                                                                                                                                                                                                          AAY39804;
                                                                                                                                                                                                                                                                      AAY39804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creutzfeldt-Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                               بر
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                                                                                                                                                                                                                                                                                                                                          sequence is 40 amino acids of the beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-571686/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Page 87; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kuru.
                                                                                                                                                                             protein, Beta/A4 amyloid (1-40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snow AD;
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0077924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US05438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; Gertsmann-Straussler syndrome
                                                                                                                                                                                                                                                                   peptide;
                                                       encephalopathy; therapy
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 209; DB 20; 100.0%; Pred. No. 3.5e-24; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein. Alzheimer's
                                                                                                                                             joint swelling;
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                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                  Fever;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated with long-standing inflammation, various forms of malignancy (including B-cell type malignancles), Familial Mediterranean Fever, multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal tunnel syndrome, joint swelling, multiple spontaneous fractures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a method for treating amyloidosis, including Alzheimer's disease
                                                                      Goyal S,
                                                                                                                 (HMRI)
                                                                                                                                                                17-JUL-1996;
                                                                                                                                                                                                              17-JUL-1996;
                                                                                                                                                                                                                                                         06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 Amyloid protein; beta-A4 therapeutic drug; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY25135 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Creutzfeldt-Jakob disease, Gerstmann Strausiler Syndrome, and other subacute spongiform encephalopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiolucency in the wrist and hip, endocrine tumours, medullary of the thyroid, diabetes, Alzheimer's disease, Down's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compositions may be useful for treating or preventing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amyloidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-561062/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1992;
23-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amyloid
                                                                                                                    HOECHST MARION ROUSSEL
                                                                      Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-8 amino acids useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĄΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-A4
                                                                      JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0969734
92US-0950417
                                                                                                                                                                96US-0682245
                                                                                                                                                                                                              96US-0682245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67-68;
                                                                      Riedel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                   peptide; aggregation; screening; inhibition;
Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83pp; English.
                                                                      NG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                      Sahasrabudhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-amyloid protein.
or preventing a form ousing this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medullary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amyloidosis
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0;

WPI; 1999-403957/34

Disclosure; Column

5-6;

8pp;

English.

Determination of degree identifying therapeutic

of aggregation of a peptide, useful for drugs for treating Alzheimer's disease

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RESULT ANTHONY AND ANTHONY AND ANTHONY AND ANTHONY AND ANTHONY AND ANTHONY AND ANTHONY ANTHONY
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Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method for the determination of the degree of aggregation of an amyloid beta A4 peptide (I) in solution. Determination comprises: (a) incubating a sample of unaggregated (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated (I); (b) measuring the amount of (II) bound to (I) to obtain a value (i); (c) repeating steps (a) and (b) with a second sample at a different time to obtain a second value (ii); and (d) determining the difference between (i) and (ii) which is inversely related to the degree of aggregation of (I). This method may be applied to a screen for compounds that inhibit aggregation of (I). These inhibitors may be used as therapeutic drugs to inhibit the
This sequence represents a fragment of the human beta-amyloid protein, and can be used in the method of the invention. The method is for inducing amyloid plaque deposition in a mammal by infusing into the brain an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque deposition has been induced are models of human Alzheimer's disease (AD) and are used to screen for agents (A) that inhibit: (a) deposition of amyloid plaque; and (b) AD-associated disruptions to sleep and circadian activity. They may also be used to study the etiology of AD. Compared
                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                        agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-amyloid;
induction; AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                     Majocha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MIRI-) MIRIAM HOSPITAL LIFESPAN PARTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease
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                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                      ng amyloid plaque deposition against Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
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                                                                                                                                                                                                                                  Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; a; sleep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                  30; 43pp;
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; circadian activity; circadian rhythm disturban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                     BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 209; DB 20;
Pred. No. 3.5e-24;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Å
                                                                                                                                                                                                                                                                                                                 in a
                                                                                                                                                                                                                                                                                                                 mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of patients
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                                                                                                                                                                                                                                                                                                                   used
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                                                                                                                                                                                                                                                                                                                 screen
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                                                                                                                              the brain
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Mismatches

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RESULT
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Matches 40
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Matches 40
                                                                                                          This sequence corresponds to an aggregating amyloid-beta peptide which can be covalently labelled with a fluorescent group. The detection or monitoring of an amyloid aggregate in a sample can be used to diagnose or detect a predisposition to Alzheimer's disease. The screening assays can be used to identify compounds for the treatment or amelioration of Alzheimer's disease or its symptoms. The fluorescent derivatives of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   any, plaques and does not stimulate an immune response. Most (I)-treated animals develop AD-type pathology (contrast transgenic models of the disease), including sleep and circadian rhythm disturbances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with known methods for inducing plaque deposition, this process causes less mechanical damage; the vehicle used is less neurocoxic and at basipH (I) is soluble enough for delivery by continuous infusion with effective delivery to brain tissue. The control peptide causes few, if
                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                    amyloid-beta peptide amyloid structure.
                                                                                                                                                                                                                                                                                                                                                                                                       WO9908695-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type aggregating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW99584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99584 standard;
                                                             Sequence
                                                                                                                                                                                                 Example 1; Page 21; 50pp; English
                                                                                                                                                                                                                          New fluorescent labeled amyloid A-beta peptides
                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                              14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                    13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aggregation; amyloid-beta peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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h 100.0%;
Similarity 100.0%;
40; Conservative (
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                                                                                                                                                                                                                                                                             Glabe
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             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 209; DB 20;
Pred. No. 3.5e-24;
; Mismatches 0;
                                                                                                 useful
209; DB 20;
No. 3.5e-24;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluorescent group; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                  for
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Best Local (
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening
effect on
                                                                                                                                                                                                                                                                                                            a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inherited congophilic angiopathy with cerebral haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
         Amyloid beta; abeta; deoxygenated solvent; evaporative deposition; research; neurotoxicity; free-radical; glutamine synthetase.
                                          Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
                                                                  28-JAN-1999
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                               This invention
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yankner
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27-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5876948-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW92723 standard;
        research;
                                                                                           AAW81473;
                                                                                                               AAW81473 standard;
                                                                                                                                                                                                                                                                                                      beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tachykinin agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hereditary
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                                                                                                                                                                       1999-189630/16
                                                                                                                                                                                                                                                                                                                                                                                                                    1b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tachykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA;
                                                                                                                                                                                                                                 Similarity
        neurotoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                    Column 41-42; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          for neurotoxin inhibitors - by testing compounds for their beta-amyloid peptide neurotoxic effect on neuronal cells
                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerebral
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                   peptide
                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0737371.
90US-0559173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agonist
                                                                                                               peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-amyloid; inhibition; neurotoxin; treatment;
; Down's Syndrome; amyloidosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                     fragments.
                                                                                                                                                                                                                                                                                                                                                                                            a method for screening compounds for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-amyloid
                                                                                                               40
                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                               Score 209; DB 20;
Pred. No. 3.5e-24;
                                                                                                                Ą
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-inherited
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       glutamine synthetase
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                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          congophilic angiopathy
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                                                                                                                                                                                                                     Gaps
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Query Match
Best Local :
                                                                                                                        sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in test to determine free-radical generating capacity and glutamine synthetase
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                              solvent treatment, useful for studying neurotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                inactivation.
                     Local
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                                                                                                                                                                                                                                                                                                                               5; Columns 11-12; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                               for treating synthetic amyloid beta peptides
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                 100.0%;
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Score 209; DB 20;
Pred. No. 3.5e-24;
0; Mismatches 0;
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                                                                    AAE05483 standard; peptide; 40
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40; Conserv
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Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive; neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension; age-related cognitive function loss; senile dementia; Wilson's disease; parkinson's disease; amylotrophic lateral sclerosis; cerebroprotective; cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia; Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma; Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease; Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease; myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke; Gilles de la Tourette's syndrome; nootropic; chronic seizure disorder; brain trauma; spinal cord trauma; acquired immunodeficiency syndrome; AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological; autonomic function disorder; Freidrich's ataxia; schizophrenia; therapy; vasotropic; neuroprotective; anti-HIV; human immunodeficiency virus; anticonvulsant; epilepsy; neuroleptic; immunostimulant. stroke;

Human peptide antigen comprising beta amyloid (Abeta) 40

24-SEP-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local Similarity
Matches 40; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to pharmaceutical compositions comprising complexes of heat shock proteins (haps) in association with antigenic molecules for use in treatment and prevention of neurodegenerative disorders and diseases. The complexes of hsp and antigenic peptides are used as vaccines for the treatment or prevention of neurodegenerative disorders e.g. Alzheimer's disease, age-related loss of cognitive function, senile dementia, parkinson's disease, amylotrophic lateral sclerosis, Wilson's disease, cerebral palsy, progressive supranuclear palsy, Guam disease, Lewy body dementia, prion diseases, spongiform encephalographics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat shock protein and antigenic molecule complexes, useful for the prevention and treatment of neurodegenerative disorders e.g. senile dementia, Alzheimer's disease and epilepsy -
             08-DEC-2000; 2000WO-US33203
                                                                           WO200142306-A2
                                                                                                                                                         Beta-amyloid
                                                                                                                                                                                    Partial sequence of a human beta-amyloid precursor protein.
                                                                                                                                                                                                                                                                                   AAB84426 standard; peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemia, glaucoma, autonomic function disorder, hypertension, neuropsychiatric disorder, schizophrenia or schizoaffective disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 13; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-451897/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000; 2000US-0489216
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                                           14-JUN-2001.
                                                                                                                                            vaccine
                                                                                                                                                                                                                                                       AAB84426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide antigen
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                                                                                                                                                                                                                                                                                                                                                                eliciting an immune response. The present s antigen comprising beta amyloid (Abeta) 40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                      precursor protein; APP; chimeric peptide; B cell epitope;
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 209; DB 22; 100.0%; Pred. No. 3.5e-24; tive 0; Mismatches 0;
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                                                                                           beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a N-CC chimeric peptides contain a N-CC chimeric peptides contain a N-CC creaminal peptide cleavage product of a precursor or mature protein, as a free N- or C-terminus, joined to a T cell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betaAPP peptides cleavage product the accumulation of amyloid beta peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They calso block the interaction of amyloid beta peptides with other molecules that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide; humans against the free N- or C-terminus of an errocursor protein or a mature product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to T cell
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-381648/40
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AA;
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AAB91780
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Best Local S
Matches 40
AAB91780 standard;
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                                                             1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvggvv 40
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                                                                                                     Similarity
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Peptide;
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                                                                                         Score 209; DB 22;
Pred. No. 3.5e-24;
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AAB91780; 22-JUN-2001 (first entry)

Amyloid beta-protein fragment peptide SEQ ID NO:956

Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter

Synthetic.

WO200069900-A2

23-NOV-2000

17-MAY-2000; 2000WO-US13576.

17-MAY-1999; 10-SEP-1999; 15-OCT-1999; 99US-0134406. 99US-0153406. 99US-0159783.

(CONJ-) CONJUCHEM INC

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Search completed: April 24, 2002, 09:17:36
Job time: 140 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a creative group (II) (e.g. succinimidyl and maleimido groups) attached to calest therapeutically active amino acid region (IV), which covalently composed so the peptides of a second to form a composed of a second to form a competitive peptides of a second acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth cale factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent caministration due to rapid degradation by peptidess in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or creduces the action of peptidases to increase length of activity (half cc life) and specificity as bonding to large molecules decreases. CC intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the cx and complete the present invention.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 506; 733pp; English.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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US-08-235-400-2
US-08-304-585-1
US-08-304-585-1
US-08-303-3734-1
US-08-633-734-1
US-08-682-245A-2
US-08-682-245A-2
US-08-98-6-448-1
PCT-US92-067700-1
US-08-302-808-4
US-08-98-454-3
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RESULT 1  US-07-744-767A-1  Sequence 1, Applic  Patent NO. 5434050  GENERAL INFORMATI  APPLICANT: Mag  APPLICANT: Mag  TITLE OF INVENT  TITLE OF INVENT  NUMBER OF SEQUE  COMPACTOR OF SEQ		45	44	43	42	41	40	39	38	37	36	35 5	34	ω	32	31	30	29	28	
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SULT 1 -07-744-767A-1 -07-744-767A-1 Sequence 1, Application US/07744767A Sequence 1, Application US/07744767A GENERAL INFORMATION: APPLICANT: Maggio, John E. APPLICANT: Mantyh, Patrick W. APPLICANT: Mantyh, Patrick W. TITLE OF INVENTION: for Use in D NUMBER OF SEQUENCES: 3 CORRECTOR NEWS 1000-1000-1000-1000-1000-1000-1000-100		100.0	100.0		100.0	•	•	100.0	100.0	100.0	100.0	100.0	•	100.0	100.0	100.0	100.0	100.0	100.0	
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myloid Peptide and etecting Alzheimer	ALIGNMENTS	US-08-976-179-1	US-08-404-831-1	US-08-467-607-1	US-08-079-511-1	US-08-302-808-6	US-08-437-067-1	US-08-235-400-1	PCT-US93-00325-1	PCT-US92-06700-2	US-09-005-215-20	US-09-388-890-1	US-08-717-551A-2	US-08-986-948-5.	US-08-682-245A-4	US-08-422-333-4	US-07-737-371E-72	US-08-609-090-9	US-08-433-734-2	
Methods 's Disease		1,	1	1,	1,	6,	1,	1,	1,	2, 1	20,	-ب	2,	5	4,	4	72,	φ,	Sequence 2, Appli	

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-744-767A-1
                                                                           Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,767A
FILING DATE: 13-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                               TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, L.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402
COMPUTER READABLE FORM:
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Similarity
                                                                                                                                                                                                                                                   40 amino acids
                                                                       100.0%; Score 209; DB 1; ilarity 100.0%; Pred. No. 2.3e-25; Conservative 0; Mismatches 0;
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US-08-235-400-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08476464A Patent No. 5707821
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Patent No.
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATOMENEY/AGENT INFORMATION:
NAME: GBylo, Paul J.
REGISTRATION NUMBER: X-95
TELECOMMUNICATION INFORMATION:
TELECHON: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: Zimmerman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: RYDEL, RUSSELL E. APPLICANT: DAPPEN, MICHAEL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                           COUNTRY: U.S.A. ZIP: 94111-3834
                                                                                                                                                                             ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
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o. 5552426
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Lilly Corporate Center/1104
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A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
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Pred. No. 2.3e-25;
Pred. No. 2.3e-25;
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Best Local Similarity
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                                                                                                 TELEFAX: 612-305-1228 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Maggio, JO
APPLICANT: Mantyh, P.
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
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ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 12-SEF CLASSIFICATION: 435
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              STRANDEDNESS:
TOPOLOGY: not
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                                                               LENGTH:
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P.O. Box 581415
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Patrick W.
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Pred. No. 2.3e-25;
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; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-302-808-3
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Best Local Similarity
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                                           MOLECULE NO HYPOTHETICAL: NO
                                                                                                                                                                                                      REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 44
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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ADDRESSEE: DIKE, BRO
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APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTINE
TITLE OF INVENTION: DERIVA
                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                              MOLECULE TYPE:
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APPLICATION NUMBER: 01013
APPLICATION NUMBER: 01013
APPLICATION NUMBER: 01013
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RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 0190
FILING DATE: 05-FEB-1993
                                                                                               TOPOLOGY:
                                                                                                          LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 3347 FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 2869 FILING DATE: 16-NOV-1993
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                                                                                                                                            ENGTH:
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                                                                                               linear
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                                 N-terminal
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Pred. No. 2.3e-25;
); Mismatches 0;
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Query Match

100.0%;

Score 209;

DB 1;

Length 40;

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-433-734-1
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                                                  ; Patent NO. 5840838
; GENERAL INFORMATION:
APPLICANT: HENSLEY,
APPLICANT: BUTTERFIE
APPLICANT: CARNEY, J
APPLICANT: AKSENOV,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08433734 Patent No. 5837473
                                                                                                                                                                                                      Sequence 8, Application US/08609090
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Best Local Similarity
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APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled
TITLE OF INVENTION: for Use in
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/433
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                       1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 amino acids
                                                  AKSENOV, Michael

VENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

VENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
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                                                                                                         BUTTERFIELD, D. A. CARNEY, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612-305-1228
                                                                                                                                                  HENSLEY, Kenneth
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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LOWE PRICE LEBLANC & BECKER
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                                                                                                                                                                                                                                                                                                                                                                                             Score 209; DB 2; Pred. No. 2.3e-25;
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Mismatches 0;
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Detecting Alzheimer's Disease
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                              APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               ZÍP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
CÓMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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STREET: 42.
STRY: Boston
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TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
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               NAME: Freeman, John W. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 amino acids
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SCREENING METHODS TO IDENTIFY
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               00108/028002
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US-08-682-245A-2
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                    TELEFAX: 513-948-7961
TELEX: 214320
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: THEST INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/682,245A
FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                         TELEPHONE: 513-948-7369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BA4 PEPTIDE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GOYAL, SHEFALI APPLICANT: PAUL, JOSEPH W
             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RIEDEL, NORBERT G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 40 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: HR
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2110 E. CITY: CINCINNATI
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                                              STRANDEDNESS:
                                                                                                                                                                                                                                 NAME: LENTZ, NELSEN L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: HOECHST MARION ROUSSEL, INC. STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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45215-6300
                                                                   amino acid
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                                                                                       40 amino acids
                                                                                                                                                          513-948-7961 OR 4681
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Pred. No. 2.3e-25;
D: Mismatches 0;
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Query Match
Best Local Similarity
Matches 40; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Score 209; DB 2; Pred. No. 2.3e-25; ; Mismatches 0;

Length 40; Indels

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                                                                                                     ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-986-948-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-986-948-3
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                             Matches
                                                        Query Match
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                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-7400
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: 08/302,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JF
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132
FILING DATE: 25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SUZUKI, NO. 595
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
                                                                                                                                                ANTI-SENSE:
                                                                                                                                                           MOLECULE TYPE: po
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 28698
APPLICATION NUMBER: 28698
APPLICATION NUMBER: 16-NOV-1993
                                                                                                                                                                                                                                                                    TELEFAX: 61, TELEFAX: 61, TELEFAX: 61, TELEFAX: 200291 STRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 0190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                           Local Similarity
                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                      LENGTH:
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                              Conservative
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100.0%; Pr
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                        Score 209; DB 4; ...
Pred. No. 2.3e-25;
Pred. No. 2.3e-25;
                                                       Length 40;
                             Indels
                           0;
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                                                                                                                                                                            RESULT
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                                                                                                       Sequence 1, Application US/08959148 Patent No. 6172277 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
APPLICANT: Tate, Barbara A.
APPLICANT: Majocha, Ronald
APPLICANT: Medocha, Ronald
APPLICANT: Newton, Julie L.
TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
FILE REFERENCE: 04930/022001
CURRENT APPLICATION NUMBER: US/08/959,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct) TELEFAX: 1-206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC/386 Compatil OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows-t CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: September 2 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette-5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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STREET: Seattle
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DESCRIPTION:
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REFERENCE/DOCKET NUMBER: UOFW-1-6707
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{SYMBOL 98 \f "Symbol"}/A4(1-40);
FIGURES 23-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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07/950,417
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Pred. No. 2.3e-25;
Mismatches 0;
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; LENGTH: 40 ; TYPE: PRT ; ORGANISM: Homo sapiens US-08-959-148-1

CURRENT FILING DATE: 1997-10-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                            ATTÓRNEY/AGENT INFORMATION:

NAME: KOWALCHYK, ALAN W.
RÉGISTRATION NUMBER: 31.535

RÉFERENCE/DOCKET NUMBER: 600.226-WO-01

TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300

TELEPHONE: (612) 332-9081

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
                              Matches
                                             Best
                                                        Query Match
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FRAGMENT TYPE:
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APPLICANT: Maggio, John E.
TITLE OF INVENTION: Labell
TITLE OF INVENTION: and A
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                            Local
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CLASSIFICATION:
                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: POFILING DATE: 19920810
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                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                 ENGTH:
                              1 Similarity
40; Conser
                                                                                                                                                                                                                                                                  AMINO ACID
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                                                                                                                                                                                                                                                                                 40 amino acid residues
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                              Conservative
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                                                                                                                    Represents isolated internal sequence of 40 amino acid residues from the -amyloid peptide precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Northgate 386
                                                                                                                                                             Internal fragment of the amyloid peptide precursor
                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merchant & Gould
                                                                                                                                                                                                         Internal Fragment Synthetically Derived
                                                                                                                                                                                                                                      Peptide
                                                                                                                 -amyloid peptide precursor
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tive 0;
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                             Score 209; DB 5;
Pred. No. 2.3e-25;
Mismatches 0;
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Pred. No. 2.3e-25;
Mismatches 0;
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                                                       Length 40;
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US-08-302-808-4
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                                                                                                                ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-302-808-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08302808 Patent No. 5750349
                                         Matches
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION.
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCT/JP94/00089
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
O10132/1993
                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                         MOLECULE TYPE:
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APPLICATION NUMBER:
FILING DATE: 16-NOV-
APPLICATION NUMBER:
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STREET:
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TELEX: 200291 STRE
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                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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                                                                                                                                                            NO
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                                         Conservative
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                                                                                                                                             N-terminal
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                                                                                                                                                                                                                  single
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                                                       100.0%;
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                                                                                                                                                                                                                                                                               4:
                                         0;
                                       Score 209; DB 1;
Pred. No. 2.4e-25;
Mismatches 0;
                                                                     Length 41;
                                         Indels
                                       0;
                                         Gaps
                                         0;
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SOFTWARE: PATENTI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PATOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEFAX: 513-948-7961 OR 4681
TELEFAX: 214330
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
STRANDEDNESS:
                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-682-245A-3
Search completed: April 24, 2002, 09:18:15 Job time: 174 sec
                                                                                                                 Вb
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US-08-682-245A-3
                                                                                                                                                                                               Query Match 100.0%; Score 209; DB 2; Best Local Similarity 100.0%; Pred. No. 2.4e-25; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08682245A
Patent NO. 5919631
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOVAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BA4 PEPTIDE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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                                                                                                       Length 41;
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0;

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Total number of hits satisfying chosen parameters:
                                                                                                                        Scoring table:
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209
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                                                 219241 seqs, 76174552 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                         DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

seq

length: 0 length: 2000000000

pir1:\*
pir2:\*
pir3:\*

Database

PIR\_68:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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B64105	S55669	T01547	PC1072	C70940	D75449	T51920	F86805	G69525	T18232	F70132	F70979	H72128	C86495	JT0959	T02581
naphthoate synthas	tegument protein 7	probable phospholi	nuclear inclusion	probable cobQ prot	sugE protein - Dei	probable xanthine	cation transporter	formylmethanofuran	conserved hypothet	conserved hypothet	hypothetical prote	3-methyl-2-oxobuta	hypothetical prote	polyprotein - pota	nodulin-like prote

# ALIGNMENTS

A;Molecule type: mRNA A;Residues: 1-57 <50Hz A;Residues: 1-58 + 50Hz A;Cross-references: EMBL:X56130 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno Blochem. Blophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra A;Reference number: PNO512; MUID:93290653
A;Accession: PNO512
A;Accession: PNO512
A;Molecule type: protein A;Residues: 1-42 <SHIv
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; amyloid Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
Brain Res. Mol. Brain Res. 10, 299-305, 1991 RESULT E60045 beta-amyloid protein - guinea pig (fragment)
C;Speciles: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999
C;Accession: pN0511
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya DЬ Qy A;Reference number: A60045; MUID:92017079 A;Accession: E60045 Query Match 100.0%; Best Local Similarity 100.0%; Matches 40; Conservative 0 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40  $\vdash$ DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40 Similarity 100.0%; 0; Score 209; DB 2; Pred. No. 3.2e-21; Mismatches 0; Score 209; DB 2; Pred. No. 2.3e-21; Mismatches 0; Length 57; Length 42; Indels Indels 0; 0, Gaps Gaps 0; 0;

a

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Alzheimer's disease
C;Species: Bos primi
C;Species: 01-Dec-1992
C;Date: 01-Dec-1992
C;Accession: D0045
                                                                            A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein;
C;Keywords: alternative splicing; Alzheimer's disease; ar
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A;Title:|Conservation of the sequence of the Alzheimer's disease amyloid peptide A;Reference number: A60045; MUID:92017079
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
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Alzheimer's disease amyloid beta/A4 protein precursor -
Alzheimer's disease amyloid beta/A4 protein precursor -
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text
C:Accession: G60045
C:Accessio
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A; Title: Conservation of the sequence of the Alzheimer's A; Reference number: A60045; MUID:92017079
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-57 <JOH>
                                                                                                                                                                                                                                                                                          A; Title: Conservation of the sequence of the Alzheimer's disease A; Reference number: A60045; MUID:92017079
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A; Residues: 1-57 < JOH>
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Bos primigenius taurus (cattle)
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Pred. No. 3.2e-21;
; Mismatches 0;
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Pred. No. 3.
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C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of t
A;Reference number: PQ0438; MUID:93075180
                                                                                                                                                                             Alzheimer's disease amyloid A4 protein precursor - C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995
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R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid A;Reference number: A60045; MUID:92017079
A;Accession: A60045
                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease amyloid beta/A4 pro
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision
                                                                                                                                                                C;Superfamily: Alzheimer's disease amyloid beta protein; animal C;Keywords: alternative splicing; Alzheimer's disease; amyloid;
                                                                                                                                                                                                                                                                                                                                C; Accession: A60045
R; Johnstone, E.M.; (
                                                                                                                                                                                                    A; Cross-references: EMBL: X56125
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-57 < JOH>
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6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
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Pred. No. 3.2e-21;
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Pred. No. 3.2e-21;
                                                                         Mismatches
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R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H. Brain Res. Mol. Brain Res. 10, 299-305, 1991 A;Title: Conservation of the sequence of the A;Reference number: A60045; MUID:92017079 A;Accession: B60045
                                                                                                                                                                             A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragmen C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
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A; Residues: 1-57 <JOH>
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                                                                                                   Query Match
Best Local
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DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
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Pred.
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1.2e-21;
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19-Oct-1995

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Alzheimer's disease amyloid beta protein precursor [validated] - human N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibit N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular protein precursor splice form App(770) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000 C;Accession: S0220; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44 4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S3 R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey Maria and Maria
                                                                                                                                                                         A; Reference number: A; Accession: S02260
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome
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A; Title: Conservation of the sequence of the Alzheimer's disease amyloid
A; Reference number: A60045; MUID:92017079
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R;Johnstone, E.M.; Chaney, M.
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A; Molecule type: DNA
A; Residues: 1-82 <DAV>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form
R;Lemaire, H.G.
                                                                                                     A; Molecule type: DNA
A; Residues: 1-288, 'V', 365-770 <LEM1>
                                                                                                                                                                                                                                            R; Lemaire, H.G.; Salbaum, J.M.; Multhaup, Nucleic Acids Res. 17, 517-522, 1989 A; Title: The PreA4(695) precursor protein
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A;Title: Homology of the amyloid beta protein A;Reference number: A49795; MUID:91273117
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A; Residues: 12-68 < JOH>
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S02260; MUID:89128427
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Pred. No. 5e-20;
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Pred. No. 4.8e-21;
Mismatches 0;
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A;ACCessium. A;ACCessium. A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
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A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
A;YOShikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, N
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein
A;Toferance number: I39451; MUID:90236318
A;Cross-references: GB:S57665; NID:9236720; PIDN:AAB19991.1; PID:9236721 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Hestor, Am. J. Hum. Genet. 51, 998-1014, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, Biochem. Biophys. Res. Commun. 170, 301-307, 1990 A;Title: Expression of a normal and variant Alzheimer's beta-protein A;Reference number: A35486; MUID:90321244 A;Accession: A35486
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A;Residues: 1-70 <VOSI>
A;Cross-references: GB:M33112; NID:g178613;
A;Accession: I39451
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A; Accession: 139452
A; Status: nucleic acid sequence not shown;
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A; Residues: 689-716, 'F', 718-737 < MUR>
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                                                                                                                                                                                                                                    A; Title: A mutation in the amyloid precursor A; Reference number: I59562; MUID:92022553
                                                                                                                                                                                                                                                                                                 R; Murrell, J.; Farlo
Science 254, 97-99,
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A;Note: a mutation with 693 Gln is presented
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A; Residues: 656-737 <LEV>
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Science 248, 1124-1126, 1990
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A;Accession: A33260
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A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and
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A; Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
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Biochem. Biophys. Res. (
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A; Residues: 656-737 < JOH>
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A; Residues: 1-75 <LAF>
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B.; Benso
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Little, S.P.
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Linkage and mutational analysis of

familial Alzheimer

disease kindreds

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A; Accession: S00707
A; Molecule type: mRNA
A; Residues: 286-344, T; 365-366 <TAN2>
A; Cross-references: EMBL: x06982; NID: 928817; PIL
A; Experimental source: promyelocytic leukemia ce
A; Note: alternative splice form APP(751)
R; Bonte, P; Gonzales-references
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A; Title: Identification, tra
A;Title: A new A4 amyloid mRNA contains a A;Reference number: $00925; MUID:88122639 A;Accession: $00925 A;Molecule type: mRNA A;Residues: 1-344,'I', 365-770 <PO2>
                                                                                                                                                                                                                                                                              A;Title: Protease inhibitor A;Reference number: S00707; A;Accession: S00707
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A; Residues: 672-678 < DYR>
R; Tanzi, R.E.; McClatchey, A.I.; Lamperti,
Nature 31, 528-530, 1988
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A;Tille: Characterization and chromosomal A;Reference number: A47584; MUID:87120328
A;Accession: A47584
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A; Cross-Teferences: GB: Y00264; NID: 928525; PIDN: CAA68374.1;
A; Note: alternative splice form APP(695)
R; Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.N.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A; Title: Molecular cloning and characterization of a cDNA er A; Reference number: A29030; MUID: 87231971
A; Accession: A29030
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A; Title: The precursor of Alzhelmer's disease amyloid A4 prot A; Reference number: A03134; MUID:87144572
A; Accession: A03134
                                                                                                               R;Ponte, P.; Gonzalez-DeWhitt,
Nature 331, 525-527, 1988
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A; Molecule type:
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A; Cross-references: GB: M16765; NID: 9178539; PIDN: AAA51722.1; A; Note: the authors translated the codon GAG for residue 647 R: Goldqaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.;
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A; Residues: 674-703 <TAN1>
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A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
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A; Residues: 687-718
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A; Residues: 1-28
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                                                    A; Cross-recervation Brain
A; Experimental source: brain
A; Experimental source: brain
R; de Strooper, B; van Leuven, F.; van den B
R; de Strooper, B; van Leuven, F.; van den B
Biochim. Biophys. Acta 1129, 141-143, 1991
A; Title: The amyloid beta protein precursor
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R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, Biochem. Biophys. Res. Commun. 149, 665-671, 1 A;Title: Complementary DNA for the mouse homol A;Reference number: A27485; MUID:88106489

homolog

of.

the

amyloid

beta

protein

, T.; 1987

A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568;

Berghe,

PIDN:AAA37139

PID: g30908

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proteinase

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mouse

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A; Accession: A27485

A; Accession: S1972 A; Molecule type: n A; Residues: 1-210, A; Reference number: A; Accession: S19727

mRNA 0,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695

<STR>

C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999 C;Accession: A27485; S19727; I49485 R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

N; Alternate C; Species: M

Species: Mus musculus (house mouse)

disease amyloid beta/A4 names: proteinase nexin

protein II

homolog

precursor

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A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573 A;NOte: the authors translated the codon GAA for residue 599 as Gly, ACC f 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT A;Note: the cited Genbank accession number, J03594, is not in release 101. R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.;
                                                                                                                                                                                                                                                                                                       A; Residues: 606-770 <VIT3>
R; Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, A; Title: Molecular cloning of amyloid cDNA A; Reference number: A31087; MUID:88124954 A; Accession: A31087
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A; Residues: 507-770 <ZAI>
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A:Residues: 122-288,'V',365-770
A:Accession: C30320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X06989; EMBL:Y00297; A;Note: alternative splice form APP(751) R;Kitaguchi, N; Takahashi, Y; Tokushima, Y Nature 331, 530-532, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with
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A; Residues: 284-288,'V', 365-770
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A; Reference number: A38949; MUID:88122641
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                                        1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
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Res. 4, 121-131, 1988
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No. 5.6e-20;
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proteinas

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A.Title: The beta-A4 amyloid precursor protein binding to copper.
A.Reference number: $46251; MUID:94320627
A;Reference number: $46251; MUID:94320627
A;Reference number: solated but not sequenced
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain A;Reference number: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is checkeywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>
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A;Reference number: 149485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 119 <RES>
A;Cross-references: GB:D10603; NID:9220328; PIDN:BAA0 C;Genetics:
A;Map position: 16C3
C;Repywords: alternative splicing; amyloid; transmembr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possit
A;Reference number: A41245; MUID:88264430
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'x','39-40,'x','42-44 <SCH>
A;Residues: 18-37,'x', dasters, C.L.; Multhaup,
FEBS Lett. 349, 109-116, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1999 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Sec
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern
A;Reference number: S00550; MUID:88312583
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <BUIL
A;Creece Formans
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R;Izumi, R.; Yamada, T.; Yoshikai,
Gene 112, 189-195, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
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92.5%;
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Pred. No. 1.8e-17;
1; Mismatches 2
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L.8e-17;
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                                                                  C;Species: potato virus Y, PVY
C;Date: 19-May-1994 #sequence-virus 19-May-1994
C;Accession: S11435; S11549; JC1526
R;Zhou, X.R.; Fang, R.X.; Wang, C.O.; Mang, K.Q.
Nucleic Acids Res. 18, 5554, 1990
A;Title: CDNA sequence of the 3'-coding region of PA;Reference number: S11435; MUID:91016851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S23094
R; KOjima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A; Title: Two-way cleavage of beta-amyloid
A; Reference number: S23094; MUID:92316198
A; Accession: S23094
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A; Molecule type: mRNA
A: Residues: 1-327 < ZHO1>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
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                                         A; Reference number: S11435; A; Accession: S11435
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A; Residues: 1-747 < OKA>
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Matches 25; Conserv
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Pred. No. 2.7e-11;
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Pred. No. 1.9e-17;
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                                                                                         Chinese isolate)
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proteinas

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A:Cross-references: EMBL:X54058
R:Zhou, X.R.
submitted to the EMBI Data Library, July 1990
A:Reference number: $11549
A:Reference number: $11549
A:Reference number: $11549
A:Reference number: $11549
A:Reference : EMBL:X54058; NID:g61219; PIDN:CAA37993.1; PID:g833159
A:Rocession: $151549
A:References: EMBL:X54058; NID:g61219; PIDN:CAA37993.1; PID:g833159
A:Rocession: $1540, YE., 92-327 < ZHO2>
A:Cross-reference number: JC1526
A:Rothshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.
Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991
A:Title: Comparison of Biological properties, serological characteristics and amino acid A:Reference number: JC1526
A:Rotession: JC1526
A:Reference number: JC1526
A:References: EMBL:X54058; NID:g6127 < OHS>
A:Title: Comparison of Biological properties, Serological characteristics and amino acid A:JC1526
A:References: EMBL:X54058; NID:g6121, YC1526
A:References: Local protein properties, Serological characteristics and amino acid A:JC1526
A:References: EMBL:X54058; NID:g6121, YC1526
A:References: Local protein properties, Serological characteristics and amino acid A:JC1526
A:References: Local protein properties, Serological properties, Serological characteristics and amino acid A:JC1526
A:References: Local protein properties, Serological properties, Serological characteristics and amino acid A:JC1526
A:References: Local properties, Serological propert
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 24, 2002, 09:16:11; Search time 62.94 Seconds (without alignments) 92.960 Million cell updates/sec

US-09-689-469-3 209 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLAVGGVV 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_17:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fung:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
5: sp\_mammal:\*
5: sp\_mammal:\* 10: Sp\_plant:\*
11: sp\_rodent:\*
12: sp\_virus:\*
13: sp\_vertebrate:\*
14: sp\_unclassified:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	P78438 homo sapien	016014 homo sapien		Q16020 homo sapien	093296 qallus qall	Q9pvll gallus gall	Q60496 cavia porce	Q9dqj8 gallus gall	Q9dqi7 qallus qall	Ogtuio sus scrofa	Q13778 homo sapien	035463 cricetulus	Q99k32 mus musculu	Q98sg0 xenopus lae	P97487 mus musculu	Q91963 xenopus lae	098sf9 xenopus lae	057394 narke japon	Q9uc33 homo sapien
B ID	4 P78438	4 Q16014	4 Q16019	4 016020	13 093296	13 Q9PVL1	11 Q60496	13 Q9DGJ8	13 Q9DGJ7	6 Q9TUI0	4 Q13778	11 035463	11 Q99K32	13 Q98SG0	11 P97487	13 Q91963	13 Q98SF9	13 057394	4 Q9UC33
% Query Match Length DB	82	82	82	82	534	269	695	695	751	770	97	79	607	693	695	747	695	669	33
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.2	6.06	6.06	6.06	6.06	6.06	89.5	86.1	84.2
Score	209	209	209	209	209	209	209	209	209	209	199	190	190	190	190	190	187	180	176
Result No.	П	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19

HSSP; P05067; 1BA4.

DR

7 79.9 780 13 073683 78.0 737 13 093279 7 70.3 28 4 0910201 5 50.1 19 6 097917 6 50.7 19 6 097917 7 7 7.3 28 4 0910201 8 50.1 19 6 097917 7 27.3 195 10 022662 7 27.3 195 10 022662 8 6 6 8 755 2 09R472 8 6 6 6 78 2 09R474 8 755 2 09R474 8 756 10 097676 8 757 2 09R474 8 758 2 09R47	780 13 780 13 780 13 780 13 781 13 781 13 782 10 782 10 783 12 783 12 783 12 783 12 783 12 784 10 785 2 785 2 786 2 78	073683 tetraodon f 093279 fugu rubrip 09uca9 homo sapien	0919e7 brachydanio 09ucdl homo sapien	097917 bos taurus	Q9ucc8 homo sapien	Ogawb6 lycopersico	022662 arabidopsis	Q9dqn5 potato viru	Q9wq05 potato viru	O81120 lotus japon	Q9r717 agrobacteri	Q9r694 agrobacteri	Q9r472 agrobacteri	O84344 chlamydia t	Q44388 agrobacteri	Q9pk54 chlamydia m	Q9xgt0 gossypium h	P93745 arabidopsis	P93733 arabidopsis	Q85276 potato viru	Q9ca59 arabidopsis	O50548 thermotoga	080960 arabidopsis
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# ALIGNMENTS

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Wed Apr

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NCBI_TaxID=9031;
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MEDLINE-9236601; PubMed-8476439;
Dennam R.B., Rosenzowaig R., Miller D.L.;
Maystem for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
Blochem. Blochem. Blochem. Blochem. 192:96-103(1993).
HSSP; P05067; 1BA4.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primațes; Catarrhini; Hominidae; Homo.
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Mammalla, Eutherla, Primates, Catarrhini, Hominidae, Homo.
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                   8DA9E42B813A070E CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
                                                                           100.0%; Score 209; DB 4;
100.0%; Pred. No. 2.1e-20;
ive 0; Mismatches 0;
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NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Gallus.
                                          Gaps
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"A system for studying the effect(s) of familial Alzheimer disease;
mutations on the processing of the beta-amyloid peptide precursor.";
Biochem. Biophys. Res. Commun. 192:96-103(1993).
BISSP; P05067; 1BA4.
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Milligan C.E.,
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    Length 82;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF042098; AAC25052.1; -.
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8882 MW; F534AA5AE5D9230A CRC64;
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01-MAR-2001 (TERMBLrel. 16, Last annotation update)
BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
BETA APP.
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Last annotation update)
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                                                                                 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
  Score 209; DB 4;
Pred. No. 2.1e-20;
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Pred. No. 2.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel, 08, Created)
                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93236601; Pubmed=8476439;
100.0%; Sc
100.0%; Pr
tive 0;
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InterPro; IRR001868; A4_APP.
PRINTS; PR00203; AMYLO1DA4.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                                                                                                                      (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2001 (TrEMBLrel. 17,
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Sarasa M., Rodolosse A., Sorribas V.;
"Cloning of full-length chicken beta-amyloid precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695;
                                                                                                                                                                                                                                                                                      Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                             EMBL; X9/001.

EMBL; X9/001.

INSP: P05067; 1BA4.

InterPro: IPR001868; A4_APP.

Pfam; PF02177; A4_EXTRA; 1.

PRINTS; PR00203; AMYLOIDA4.

SMART; SM00006; A4_EXTRA; 1.

PROSITE; PS00319; A4_EXTRA; 1.

PROSITE; PS00320; A4_INTRA; 1.

PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F201ED02AEC86D95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
                                   SÜBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
                                                                                                                                                                                                                                                                                                                                                                                     597 DAEFRHDSGYEVHHQKLVFFFAEDVGSNKGAIIGLMVGGVV 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 636
                                                                                                                                                                                                                                                                                      100.0%; Score 209; DB 11; 100.0%; Pred. No. 2.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 209; DB 13;
Pred. No. 2.7e-19;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                               1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              751 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWHI. AF289218; AAGG0593.1; InterPro: IRR01868; A4_APP.
Pfam; PF02177; A4_EXTRA; I.
PRINTS; PR00203; AMYLOIDA4.
SMART; SM00006; A4_EXTRA; I.
PROSITE; PS00319; A4_EXTRA; I.
SEQUENCE 695 AA; 78565 MW; F
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100.0%;
                                                                           EMBL; X97631; CAA66230.1;
HSSP; P05067; 1BA4.
                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09DGJ8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoforms.";
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09DGJ7;
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Q9DGJ8
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
"What the evolution of the amyloid protein precursor supergene family tells us about its function.";
Neurochem. Int. 0:0-0(2000).
EMBL; AF030341; AAF12698.1; -.
HSSP; P05067; 1BA4.
InterPro; IPR001868; A4_APP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-007-1996 (TrEMBLrel. 17, Last annotation update)
01-007-2001 (TrEMBLrel. 17, Last annotation update)
01-008-2001 (TrEMBLrel. 17, Last annotation update)
01-008-2001 (TrEMBLrel. 17, Last annotation update)
01-008-2001 (Guinea pig).
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Glonodata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae, Cavia.
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0
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                                                                           Length 534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck M., Mueller D., Bigl V.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
               60597 MW; FB53ECC2E66D4C92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OAB8BB851863A19D CRC64;
                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                        436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 475
                                                                           DB 13;
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0
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                                                                                                                                                  1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.1e-19;
                                                                       100.0%; Score 209; DB 1.7
100.0%; Pred. No. 2e-19;
Tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 AA
                                                                                                                                                                                                                                                                                      569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 209;
                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last anno AMYLOID PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02177; A4 EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Conservative
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
                 534 AA;
                                                                         Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus
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Goldgaber D., Lerman M.I., McBride O.W., Safflotti U., Gajdusek D.C.; "Characterization and chronosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease."; Science 235:877-880(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA APP.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Sambanurti K., Pinnix I., Gandhi S.; Sambanurti K., Pinnix I., Gandhi S.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF030413; AAB86608.1; -- HSSP; P05067; 1QCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1996 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAR-2001 (TrEMBLrel. 16, Last annotation update)
ALZHEIMER S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AA; 10884 MW; E528CDB448DE474E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;
                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AMYLOID PROTEIN (AD-AP) (FRAGMENT).
672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%; Score 199; DB 4; 100.0%; Pred. No. 5.3e-19; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 190; DB 11;
Pred. No. 6.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87120328; Pubmed=3810169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M15533; AAA35540.1; -. HSSP; P05067; 1BA4.
                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001868; A4_APP.
PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.2
Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10029;
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SEQUENCE
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SEQUENCE
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                                                                                RESULT 11
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECURNCE FROM N.A.

Kimura A., Takahashi T.;

"Amyloid Precursor Protein 770.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-! SIMILARIY: TO PARCREATIC FRYPSIN INHIBITOR (KUNITZ) DOMAIN.

EMBL, AB022550; BAA84580.1; -.
                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO PANCERATIC TRYPSIN INHIBITOR (KUNITZ) DOMAIN.
EMBL; AF289219; AAG00594.1; -
INTERPO: IPR001868; A4_APP.
INTERPO: IPR00223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA: 1.
Pfam; PF001714; Kunitz_BPTI; 1.
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                                                           Sarasa M., Rodolosse A., Sorribas V.; "Cloning of full-length chicken beta-amyloid precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  751 AA; 84705 MW; E78E9413A8033D84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 209; DB 6; Similarity 100.0%; Pred. No. 3.1e-19; 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 209; DB 13;
11arity 100.0%; Pred. No. 3e-19;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001868; A4_APP.
InterPro; IPR00223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; I.
Pfam; PF00014; Kunitz_BPTI; I.
PRINTS; PR00203; AMXLOIDA4.
PRINTS; PR00759; BASICPTASE.
SMART; SM00006; A4_EXTRA; I.
SMART; SM00131; KU; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SETINE PIOCEASE inhibitor.
SEQUENCE 770 AA; 86961 MW; 5F7A;
                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0260; BPTLKUNITZ_1; 1.
PROSITE; PSS0279; BPTL KUNITZ_2; 1.
Serine protease inhibitor.
SEQUENCE 751 AA; B4705 MW; E78E
                                                                                                                                                                                                                                                                                                  SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
                                                                                                                                                                                                                                                           PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
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SEQUENCE FROM N.A.
NCBI_TaxID-9031;
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Gaps

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1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

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Search completed: April 24, 2002, 09:20:10 Job time: 239 sec
HIPPOCAMPAL AMYLOID PROTEIN
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Best Local Similarity
Matches 37; Conserv
                                                           NCBI_TaxID=10090;
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                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (FOVIETN FOR IMAGE:3486773) (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                       Strausberg R.;
Submitted (MAR.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005490; AAH05490.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. CAF1DF655C1AB653 CRC64;
                                                                                                                                                                                                                                        SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P97487 PRELIMINARX; PRT; 695 AA. P97487; p97487; CTEMBLEI. 03, Created) 01-MAY-1997 (TrEMBLEI. 03, Last sequence update) 01-JUN-2001 (TrEMBLEI. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN A.
                                                                                                                                                                                                                                                                                                                                         Van den Hurk W.H.;
Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
EMBL, AJ298150; CAC37193.1;
                                                                                                                                                                                                                                                                             Query Match 90.9%; Score 190; DB 11; Best Local Similarity 92.5%; Pred. No. 7.5e-17; Matches 37; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.9%; Score 190; DB 13;
87.5%; Pred. No. 8.8e-17;
Live 4; Mismatches 1;
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                                  607 AA.
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693 AA; 78568 MW;
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                                  PRELIMINARY;
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                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=10090;
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P97487
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Gaps
                      Craniata, Vertebrata, Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                   STRAIN-129SV;
Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi
Loring J.F., Goate A.M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U84012; AAB41502.1; -.
EMBL; U82624; AAB40919.1; -.
                                                                                                        SEQUENCE FROM N.A.
STRAIN=SAMP8; TISSUE-HIPPOCAMPUS;
Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
Submitted (JAN-1997) to the EMBL/GenBank/PDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                     SEQUENCE OF 581-662 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:88059; App.
InterPro; IPR001868; A4_APP.
Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

April 24, 2002, 09:16:26; Search time 21.42 Seconds (without alignments) 68.468 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-689-469-3 209 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	A4_PIG	A4_URSMA	CANFA	RABIT	SHEEP		A4_SAISC 09		SE	TI .			PSESP	_MYCPN			_PVYYO	GRT3		ORBU	ARCFU	MYCIU	_HAEIN	SEAE		SOMMO			z	HDC_DROME Q5	z	ECOLI	COAT_PEMV P(
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P54424 ustilago ma	Q03218 saccharomyc	Q02094 homo sapien	P14297 manduca sex	P43741 haemophilus	Q9gzv9 homo sapien	P77819 bacillus an	P77839 brochothrix	032227 bacillus su	Q06174 bacillus st	051581 borrelia bu	P24040 pseudomonas
GUNI_USTMA	YM43_YEAST	RHAG_HUMAN	ARYB_MANSE	DPO1_HAEIN	FGFN_HUMAN	RPOC_BACAN	RPOC_BROTH	YVAE_BACSU	EST_BACST	G6PD_BORBU	NIRS_PSEST
٠.,	7	٦	7	Н	Н	Н	П	П	٦	Н	Т
393	210	409	703	930	251	1052	1053	119	247	478	260
23.2	73.5	23.0	23.0	23.0	22.7	22.7	22.7	22.5	22.5	22.5	22.5
48.5	48.5	48	48	48	47.5	47.5	47.5	47	47	47	47
34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsitation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institutes are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Brain Res. 10:299-10:299-10:391-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:291-10:29
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG (CONTAINS: BETA-AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92017079; PubMed=1656157;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
                                                                                                                                                                                                                                                                 Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., "Conservation of the sequence of the Alzheimer's disease amyloid
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8469D488A2E12DFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 209; DB 1;
100.0%; Pred. No. 2.1e-21;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                          TISSUE=Kidney;
MEDLINE=92017079; PubMed=1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
34
58
58
6285 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X56125; CAA39590.1; -.
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                              Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P05067; 1AML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 40; Conserv
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                     NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4_RABIT
Q28748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A4_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G(O) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2000 (Rel. 35, Last amnotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE AWYLOID A4 PROTEIN HOWOLOG [CONTAINS: BETA-AWYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzhelmer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis."; the polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-i- FUNCTION: FUNCTIONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                         Ursus maritimus (Polar bear) (Thalarctos maritimus).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Ursidae, Ursus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 2.1e-21;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
G19COSTE; PS00320; A4_INTRA; PARTIAL.
G19COPCOteln; Amyloid; Neurone; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
MEDLINE-92017079; PubMed-1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56128; CAA39593.1; -. HSSP; P05067; 1AML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6172 MW;
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                                                                                                                                                                            STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29073;
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NON_TER
SEQUENCE
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Q29149;
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Q28280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 AA;
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Q28053;
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DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."; Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLURAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F434209D88EBA82D CRC64;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                      G(O) (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 209; DB 1; 100.0%; Pred. No. 2.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
G1yoprotein; Amyloid; Neurone; Transmembrane.
NON-IER
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TISSUE-Heart;
MEDLINE-92017079; Pubmed-1656157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9940;
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Q28757;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01.NOV-1997 (Rel. 35, Last sequence update)
30.MAY-2000 (Rel. 39, Last annotation update)
ALGRIEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                  BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                F434209D88EBA82D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 209; DB 1;
; Pred. No. 2.1e-21;
0; Mismatches 0;
                                                                                                                       HSSP: P05067; 1AML.
INTERPRO; IPRO01868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
G1YCOPICOLEIN; AMYloid; Neurone; Transmembrane.
CHAIN
6 48 BETA-AMYLOID PROTI
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PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DAEFRHDSGYEVHDQKLVFFAEDVGSNKGAIIGLMYGGVV
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not removed.
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                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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MEDLINE-92017079; PubMed=1656157;
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100.0%;
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                                                                                               EMBL; X56130; CAA39595.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                6300 MW;
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Best Local Similarity 100.

Matches 40; Conservative
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ACT_SITE
DISULFID
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SEQUENCE
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TRANSMEM
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-!- GOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
-!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF: THIS INTERACTION APPEARS TO BE INDEPENDENT OF
PHOSPHORYLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE APP FAMILY.
-!- SIMILARITY: CONTAINS 1 BPTIKUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sainiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebral amyloid angiopathy.";
Neurobiol. Aging 16:805-808(1995)
-!- FUNCTION: FUNCTIONAL BERCEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last amoutation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (CONTAINS: BETA-
                                                                                                                                                                                                                                  ;
                 BETA-AMYLOID PROTEIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver, and Kidney;
MEDLINE-96108492; PubMed-8532114;
Levy E., Amorim A., Frangione B., Walker L.C.;
"Beta-amyloid precursor protein gene in squirrel monkeys with
                                                                                                                                                                                          Length 59;
                                                                                                                                                                                                                                  Indels
                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                        F43469D488A2E12D CRC64;
                                                                                                                                                                                      100.0%; Score 209; DB 1;
100.0%; Pred. No. 2.1e-21;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                       DAEFRHDSGYEVHHQKLVFFAEDVGSNKCAIIGLMVGGVV 40
                                                                                                                                                                                                                                                                                                                                                                                                                          751 AA
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SMART; SM0131; KU; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_IMPRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001868; A4_APP.
InterPro; IPR002233; Kunitz_BPTI.
Pfam; PF00177; A4_EXTRA; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
                                                                                                                          6414 MW;
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
Matches 40; Conserv
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                   CHAIN
DOMAIN
TRANSMEM
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SEQUENCE
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Q95241;
NON_TER
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Kang J., Lemaire H. G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.; "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A4_HUMAN STANDARD; PRT; 770 AA.
P05067; P00000; Q16011;
13-AUG-1987 (Rel. Q5, Created)
20-AUG-2001 (Rel. 20, Last sequence update)
ALCHEDIMEN S DISEASE AMILOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-IÏ)
APP OR A4 OR CVAP OR ADI.
PROSITE; PS50279; BPT1_KUNIT2_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89128427; PubMed-2783775;
Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
"The PreA4(695) precursor protein of Alzhelmer's disease A4 amyloid in a encoded by 16 exons."
Nucleic Acids Res. 17:517-552(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-88122639; PubMed-2893289;
Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
Cordell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-97263807; PubMed-9108164;
Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (PROBABLE)
N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                      CLATHRIN-BINDING (BY SIMILARITY).
REACTIVE BOND.
                                                                                                       BETA-AMYLOID PROTEIN (POTENTIAL) EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A new A4 amyloid mRNA contains a domain homologous to serine
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                            6C3E431089569049 CRC64;
                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). BPTI/KUNITZ INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMYGGVV 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 209; DB 1;
; Pred. No. 3.1e-20;
0; Mismatches 0;
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                                                                 BY SIMILARITY.
A4 PROTEIN.
                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                         POTENTIAL.
                                               Ignal; Serine protease inhibitor.
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100.0%;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteinase inhibitors.";
Nature 331:525-527(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 40; Conservative
                                                                                     751
680
680
704
704
345
743
345
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337
523
553
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                                                                                                                                                                                                                                                                                                                                                                           751 AA;
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653
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681
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Nature 341:144-147(1989).
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     SEQUENCE OF 672-681.
MEDLINE=88035004; PubMed=3312495;
Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
Tourtellotte W.W., Huebner V., Shively J.E.;
"Amyloid angiopathy of Alzheimer's disease: amino acid composition and partial sequence of a 4,200-dalton peptide isolated from cortical
                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain; coding and nonocoding regions of the fetal precursor mRNA are expressed in the cortex.";
Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY OF APP WITH NEXIN-II.
MEDILINE-89384866; PUDMed-2506449;
Ollersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted form of the Alzheimer's amyloid precursor protein with the Kunitz domain is protease nexin-II.";
                                                                                                                                                                                                                                                                                                                                                                         Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
           "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus."; Nucleic Acids Res. 25:1802-1808(1997).
                                                           SEQUENCE OF 286-345 AND 365-366 FROM N.A.
MEDLINE-88122640; PubMed-2893290;
Tanzi R.E., Mcclatchey A.I., Lamperti E.D., Villa-Komaroff L.,
Gusella J.F., Neve R.L.;
"Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89016647; PubMed-3140222;
Schon E.A., Mita S., Sadlock J., Herbert J.;
A cDNA specifying the human amyloid beta precursor protein (ABPP)
encodes a 95-kDa polypeptide.";
Nucleic Acids Res. 16:9351-9351(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y., "Genomic organization of the human amyloid beta-protein precursor
                                                                                                                                                                                                                                                                                               the
                                                                                                                                                               SEQUENCE OF 287-367 FROM N.A.
MEDLINE-88122641; PubMed-2893291;
Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
"Novel precursor of Alzheimer's disease amyloid protein shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Nostrand W.E., Cunningham D.D.; "Purification of protease nexin II from human fibroblasts."; J. Biol. Chem. 262:8508-8514(1987).
                                                                                                                                                                                                                                                                 MEDLINE-87231971; PubMed-3035574; Kobakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; Molecular cloning and characterization of a cDNA encoding terebrovascular and the neuritic plaque amyloid peptides."; Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
                                                                                                                                                                                                                                                        SEQUENCE OF 284-289 AND 365-770 FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 507-770 FROM N.A. MEDLINE=88124954; PubMed=2893379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurochem. 49:1394-1401(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87250462; PubMed=3597385;
 Sakaki Y.;
                                                                                                                                                                                                                   protease inhibitory activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                        Nature 331:528-530(1988).
                                                                                                                                                                                                                              Nature 331:530-532(1988).
Saito M., Tsukuni S.,
"A novel method for ma
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Murayama Y., Ogata E.;
"Alzheimer amyloid protein precursor complexes with brain GTP-binding
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Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
"Solution structure of amyloid beta-peptide(1-40) in a water-micelle environment. Is the membrane-spanning domain where we think it is?";
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Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
"Three-dimensional structures of the amyloid beta peptide (25-35) in
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G., Unterbeck A.,
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                                                                       Katunuma
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Poulsen S.-A., Watson A.A., Craik D.J.;
"Solution structures in aqueous SDS micelles of two amyloid beta
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                         MEDLINE-90211252; PubMed-1969731;
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Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.
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MEDLINE=92031488; PubMed=1718421;
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Alzheimer's amyloid beta-protein precursor.";
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OF INHIBITOR DOMAIN
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MEDLINE=93188965; PubMed=8446172;
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PROTEASE-SPECIFICITY
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"Complementary DNA for the mouse homolog of the human amyloid beta
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
      Lemaire H.-G.,
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                                                                                                                                                                       Indels
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01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AWYLOID A4 PROTEIN HOWOLOG PRECURSOR
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                                                                                                      "Alzheimer's disease: a cell biological perspective."; Science 256:780-783(1992).
                                                                                                                                                                                                         672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
                                                                                                                                                100.0%; Score 209; DB 1;
100.0%; Pred. No. 3.2e-20;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                          (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-Brain; MEDLINE-92096458; PubMed=1756177;
                                                                                MEDLINE=92271194; PubMed=1589757;
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MEDLINE-89345111; PubMed=2569710;
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MEDLINE=92209998; PubMed=1555768;
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Best Local Similarity 100.
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                             Kosik K.S.;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           WITH XII -ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NEXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                             DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
                                                               Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.; "Structure and expression of the alternatively-spliced forms of mRNA for the mouse homolog of Alzheimer's disease amyloid beta protein
                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
                                                                                                                                                  Biochem. Biophys. Res. Commun. 158:906-912(1989).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(771) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
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CLATHRIN-BINING (BY SIMILARITY).
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  OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING
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SEQUENCE OF 281-380 FROM N.A., ANI
TISSUE-Brain, and Kidney;
MEDLINE-89149813; PubMed-2493250;
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PIR; S04855; S04855.
PIR; S19727; S19727.
MGD; MGI:88059; App.
InterPro; IPR0012868; A4_APP.
InterPro; IPR002223; Kunitz_Bi
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EMBL; X15210; CAA33280.1; -.
EMBL; D10603; BAA01456.1; -.
EMBL; M24397; AA3392929.1; -.
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RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ, INHIBITOR DOMAIN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Seeburg P.H.;
"Alzheimer's disease amyloidogenic glycoprotein: expression pattern
in rat brain suggests a role in cell contact.";
EMBO J. 7:1365-1370(1988).
                                                                                                                                                                                                                                                                                                                  Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
                                         ;
                   Length 770;
                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
                                         Indels
                                                                       Score 190; DB 1; I
Pred. No. 1.1e-17;
; Mismatches 2;
                                                            1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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MEDLINE=89183625; PubMed=2648331;
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InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00014; Kunitza_BPTi; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 289-364 FROM N.A.
                  90.9%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X07648; CAA30488.1; -. EMBL; X14066; CAA32229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00759; BASICPTASE. SMART; SM00006; A4_EXTRA; 1.
                                       Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S00550; S00550.
PIR; S03607; S03607.
                            Similarity
                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                         37;
                  Query Match
Best Local 9
                                                                                                                                       A4_RAT
P08592;
                                                                                                                  RESULT 10
                                      Matches
                                                                                                                             A4_RAT
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P21294;
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 40, Last annotation update)
GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA_DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                             ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
                                                                                                                                                                                                                                                                                                                       BPTI/KUNITZ INHIBITOR.
CLATHRIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E -> V (IN ISOFORM APP(695)).
MISSING (IN ISOFORM APP(695)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potato virus Y (strain Chinese isolate) (PVY).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91016851; PubMed=2216735; Zhou X.R., Fang R.X., Wang C.Q., Mang K.Q.; "cDNA sequence of the 3'-coding region of PVY genome (the Chinese
                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
EQUIVALENT OF BETA-AMYLOID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
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-1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
-1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
SMART; SM00131; KU; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00280; B4_INTRA; 1.
PROSITE; PS00799; BPTI_KUNITZ_1; 1.
PROSITE; PS50799; BPTI_KUNITZ_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; Signal; Alternative splicing; Serine protease inhibitor.
BY SIMILEMENTY.
BY SIMILEMENTY.
                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 190; DB 1; Le
Pred. No. 1.1e-17;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 DAEFGHDSGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVV 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
                                                                                                                                                                                                                                                             POTENTIAL.
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HSSP; P05067; IAMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86704
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Matches 37; Conservative
                                                                                                                                                                                                                                      699
723
715
715
345
341
334
337
571
289
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289
290
770 AA;
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700
724
673
287
759
291
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TRANSMEM
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VARSPLIC
SEQUENCE
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CHAIN SEQUENCE

Matches

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8 SGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 AA; 52156
                                                                                                                                                                                                                Pseudomonas sp.
Bacteria; Proteobacteria.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S27652; S27652.
PIR; C42971; C42971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P20000; 1A4Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                        DHAL_PSESP
P33008;
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ACT_SITE
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SEQUENCE
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DHAL_PSESP
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Y226_MYCPN
                                Dp
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SEQUENCE FROM N.A.
MEDLINE-9705159; PubMed-8896276;
Sterky F., Holmberg A., Pettersson B., Uhlen M.;
Sterky F., Holmberg A., Pettersson B., Uhlen M.;
The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes.";
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
              Pfam; PF00767; Poty_coat; 1.
Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLG1 PROTEIN.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
EEE164F2374CCCE3 CRC64;
                                                                                                                                                                    10;
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Pred. No. 3.4;
5; Mismatches 5; Indels
                                                                                                                                     Score 57; DB 1; Length 327;
Pred. No. 2.5;
                                                            NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Bettignies G., Bergez-Aullo P., Barthe C., Louvet O., Peypouquet M.F., Morel C., Doignon F., Crouzet M.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                          COAT PROTEIN.
8F8355E2DE6F2F18 CRC64;
                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) SLG1 PROTEIN PRECURSOR.
                                                                                                                         27.3%; Scur.
53.1%; Pred. No. 2..,
0; Mismatches
                                                                                                                                                                                                                                                                                                         378 AA
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InterPro; IPR001592; Poty_coat.
                                                            <1 60 NU
61 327 CC
327 AA; 36868 MW;
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EMBL; U43491; AAC49488.1; --
EMBL; Z74916; CAA9196.1; --
HSSP; P05067; IBA6.
SGD; S0005534; SLG1.
InterPro; IRPG02889; WSC.
Pfam; PF01822; WSC; 1.
                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-NOV-1997 (Rel. 35, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
MW
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42.4%;
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                                                                                                                                                                   17; Conservative
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                                                                                                                                                                                                                                                                                                       STANDARD;
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65
354 3
378 AA;
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                      SLG1_YEAST
P54867;
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92332528; PubMed-1629218;
Peterson J.A., Lu J.-Y., Geisselsoder J., Graham-Lorence S.,
Carmona C., Witney F., Lorence M.C.;
Cytcoknome P-450terp. Isolation and purification of the protein and cloning and sequencing of its operon.";
J. Blol. Chem. 267:14193-14203(1992).
-!- FUNCTION: INVOLVED IN A ALPHA-TERPINEOL OXIDATION SYSTEM.
-!- CATALITIC ACTIVITY: ALDEHYDE + NAD(+) + H(2)O = ACID + NADH.
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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P75462;
01-NOV-1997 (Rel. 35, Created)
20-AUG-2001 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MG226 HOMOLOG (F10_ORF503).
MPN319 OR MP517.
Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD (ADP PART) (BY SIMILARITY).
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Pred. No. 7;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

2144AEIEB173C854 CRC64;
                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-EB-1996 (Rel. 33, Last annotation update)
PROBABLE ALDEHYDE DEHYDROGENASE (EC 1.2.1.3).
488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002086; Aldehyde_dehydr.
Pfam: PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
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CARBOHYD SEQUENCE

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID=pTiAch5;
MEDLINE=84207942; PubMed=6327292;
Gieln J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
Lemmers M., van Montagu M., Schell J.;
"The complete nucleotide sequence of the TL-DNA of the Agrobacterium
tumefaciens plasmid pTiAch5.";
EMBO J. 3:835-846(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens.
Plasmid pTiAch5, and Plasmid pTiA6NC.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                  pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO M.GENITALIUM MG225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                      Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
4BC1BFDE036985B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 1;
Pred. No. 7.2;
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Last annotation update)
NASE (EC 1.13.12.3).
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InterPro; IPR002027; Amino_acid_permease.
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                                      SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 PC
54960 MW;
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(Rel. 02, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000051; AAB96165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00324; aa_permeases; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%;
64.7%;
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Best Local Similarity 64.7;
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NCBI_TaxID=2104;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                     PLASMID=pT1A6NC;
MEDLINE-84170374; pubmed=6584906;
Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
Fuller S., Flores C., Peschon J., Nester E., Gordon M.;
"Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti
plasmid: two gene products involved in plant tumorigenesis.";
Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
-!- CATALYTIC ACTIVITY: L-TRYPTOPHAN + O(2) = INDOLE-3-ACETAMIDE +
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9FD2B83FEA001A4D CRC64;
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InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
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755 AA;
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SEQUENCE FROM N.A.
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Search completed: April 24, 2002, 09:20:38 Job time: 252 sec

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Amyloid b Amyloid b

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AAB84430
AAW02336
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AAW81471
AAR60362
AAW92722
AAB91799
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AAY25134
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AAY52132
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AAR60364
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AAW89357
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AAB91803
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12.249 Million cell updates/sec
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| SIDS8/gcgdata/geneseq/geneseqp/AAA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Scoring table:

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Human peptide

Beta-amyloid Beta-amyloid

## ALIGNMENTS

protein; APP; Alzheimer's disease; beta-amyloid; antibody; diagnosis; immunogen; antigen; epitope. AAR60369 standard; peptide; 11 AA. Suzuki N; 93JP-0010132. 93JP-0019035. 93JP-0286985. 93JP-0334773. (TAKE ) TAKEDA CHEM IND LTD. 94WO-JP00089 (first entry) Beta-amyloid (25-35). Odaka A, WPI; 1994-264110/32 Amyloid precursor anti-beta-amyloid Homo sapiens. 24-JAN-1994; 25-JAN-1993; 05-FEB-1993; 16-NOV-1993; 28-DEC-1993; WO9417197-A. 15-MAR-1995 04 - AUG - 1994 Kitada C, AAR60369; AAR60369 RESULT THE STATE OF THE S

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as

Beta-amyloid (25-3 beta-amyloid (25-3 Human beta-amyloid Amyloid beta pepti Neurotoxic beta-am Beta-amyloid pepti

AAR87948 AAR92807 AAW23336 AAW64497 AAW47231 AAW81470

AAR60369

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DB

Length

Query

Score

Result о М

Description

Synthetic amyloid Human Receptor to Amyloid beta-prote Amyloid beta-prote Neurotoxic beta-am

AAY52133 AAB91775 AAB91808 AAW64498

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Amyloid beta peptide 2 used to inhibit damage to cells in Alzheimer's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor - used for inhibiting amyloid-beta protein neurotoxicity in e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptides PB145, PB446 and PB96 can be used to inhibit the neurotoxicity of the present peptide, beta-amyloid 25-35, and are therefore useful in the treatment of Alzheimer's disease and Down's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's disease; Down's syndrome; inhibition; neurotoxicity; beta-amyloid 25-35.
                                      Score 11; DB 16;
Pred. No. 3.9e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 11; DB 17;
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                                      100.0%;
llarity 100.0%;
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Best Local Similarity 100.

Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to new chemical compounds which are peptides of formulae XXXX (I), XXXXZ (II) and XIXXZXX (III), and peptides comprising the sequences (I), (II) or (III) and containing not greater than 8 maino acid cresidues. In the formulae, X is any maino acid with a cationic side chain, N and Z are neutral amino acids, and two of XI, XZ and X3 are amino acids with an anionic side chain and the third is an amino acid with an anionic or neutral side chain. Also new is the peptide with an anionic or neutral side chain. Also new is the peptide of Jy-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is the latter undecapeptide which represents amino acids 25-35 of the beta-amyloid peptide A-beta.

The peptides inhibit the binding of glycosaminoglycans and/or proteoglycans to A-beta peptide and hence can be used for preventing the formation of amyloid plaques and for treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                           Antibodies which recognise specific subfragments of the beta-amyloid
                                                                                            protein are claimed. Specifically, the antibodies (which are prefix monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; beta-amyloid; plaque; glycosaminoglycan;
                                                                                                                                                                                                                                                                                                Length 11;
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100.0%; Pred. No. 3.9e-06;
ive 0; Mismatches 0;
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                                      2; Page 84; 116pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-amyloid (25-35) peptide.
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Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                  disease
                                      Claim
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Gaps

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Indels

Length 11;

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16-JUL-1998
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                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAW2335-36 are portions of the the amyloid beta peptide, which is the principal component of extracellular deposits in Alzheimer's disease. It has been shown to promote nuerite outgrowth, generate reactive oxygen intermediates, induce cellular oxidant stress, lead to neuronal cytotoxcity, and promote microgilal activation. The present composition comperises and agent capable of inhibiting interaction of an amyloid beta peptide, with a receptor for advanced glycosylation end product and a carrier. A method for inhibiting interaction of anyloid beta peptide with a receptor for advanced glycosylation on the surface of a cell comprises contacting the cell with e.g. present peptide. Depending on the type of cell, inhibiting the interaction between the amyloid beta peptide and the receptor for advanced glycosylation can be used for inhibiting comparation of a neuronal cell, inhibiting formation of an amyloid beta peptide on the surface of a cell, inhibiting activation of anyloid beta ceptide on the surface of a cell, inhibiting activation of microgilal cells bettied that surface of a cell, inhibiting activation of microgilal cells bettied on the surface of a cell, inhibiting activation of microgilal cells by amyloid betta peptide. The methods can be used for tracting e.g. by amyloid betta peptide. The methods can be used for tracting e.g. cell into senile plaques, and inhibiting activation of microgilal cells by amyloid betta peptide. The methods can be used for tracting e.g. diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic can be associated with head trauma, amyotrophic lateral sclerosis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Amyloid beta peptide; extracellular deposit; Alzheimer's disease; nuerite outgrowth; microglial activation; neuronal cell degeneration; receptor for advanced glycosylation end product; amyloid beta peptide fibril.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent which inhibits interaction of an amyloid-beta peptide with a receptor for advanced glycosylation end product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 11; DB 18; 11 Similarity 100.0%; Pred. No. 3.9e-06; 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis or neuronal degeneration.
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                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 10; 91pp; English.
                                                                                                                                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                 Yan SD;
                                                                                                                                                           97WO-US00857.
                                                                                                                                                                                        96US-0592070
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                                                                                                                                                                                                                                               Schmidt AM, Stern D,
                                                                                                                                                                                                                                                                          WPI; 1997-393374/36.
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Best Local Similarity
Matches 11; Conserv
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                                                                         Homo sapiens
                                                                                                    WO9726913-A1
                                                                                                                                                          21-JAN-1997;
                                                                                                                                                                                        26-JAN-1996;
                                                                                                                               31-JUL-1997.
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Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx; aggregate; Alzheimers disease; decoy; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to form aggragates that increase calcium influx into neuronal cells. Such peptides can be used in the treatment of diseases associated with neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The peptides are administered at 0.001-1000 (especially 0.2-20) mg/Kg, by injection and orally, or from slow-release implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of aggregation of, e.g. beta-amyloid peptide - by administering decoy peptide or other calcium-influx inhibitor, useful for, e.g. treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 11; DB 19;
ilarity 100.0%; Pred. No. 3.9e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening assay; beta-amyloid peptide; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amyloidosis disease; Alzĥeimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                 (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-amyloid peptide residues 25-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 42; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47231 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                       98WO-US00653
                                                                                                                                                                                                                                                                                                            97US-0960188.
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91US-0744767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-398795/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSNKGAIIGLM 11
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blanchard BJ,
                                                                                                                                                                                                                                                                                                            29-OCT-1997;
10-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluorochanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                             New in vitro screening assay for Alzheimer's disease drugs - comprises assessing binding of labelled beta-amyloid peptide to silk
                                                                                                                                                                            The present sequence was used in the development of a novel in vitro screening assay for agents capable of affecting the deposition of beta-amyloid peptide (BAP) on tissue. The method comprises contacting a silk sample with labelled BAP, optionally in the presence of a test agent, detecting the amount of label bound to the silk and assessing the effect of the agent on the deposition of BAP. Agents that inhibit binding of BAP to silk are potentially useful for treating amyloidosis diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition; research; neurotoxicity; free-radical; glutamine synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic amyloid beta (Abeta) peptide 5 (residues 25-35).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hensley K;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 19;
Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carney JM,
                                                                                                                                                Example 1; Columns 29-30; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Columns 9-10; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW81470 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Sv
1 Similarity 100.0%; P:
11; Conservative 0;
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              Mantyh PW;
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                                                                                                                                                                                                                                                                                                                     Alzheimer's disease.
                                            WPI; 1998-168404/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSNKGAIIGLM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amyloid beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999
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              Maggio JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW81470;
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solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in test to determine free-radical generating capacity and glutamine synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble receptor for advanced glycation endproducts; RAGE; tumour:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to AGE (RAGE) amino acid sequence fragment #2.
                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invasion; metastasis; amphoterin; neuron; inhibit; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                               Score 11; DB 20;
Pred. No. 3.9e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY52133 standard; peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSNKGALIGLM 11
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                    11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Receptor
                                                                                                                                                                                                           inactivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9954485-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt AM,
                                                                                                                                                                                                                                                                           Sequence
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Sequence

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AAB91808 standard; Peptide; 11 AA.
                             1 GSNKGAIIGLM 11
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                                                                                                                                                                                                                                                                                                                 23-NOV-2000
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                             AAB91808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                         AAB91808
                                      g
                                                                                                                 The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attended to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides or 9-50 amino acids. (I) are useful for modifying therapeutic peptides or 9-60 minos, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life and specificity as bonding to large molecules adereases intracellular uptake and interference with physiological processes. AAB90829 to AAB9241 represent peptides which can be used in the cremptification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                         Gaps
                                                                                                                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thibaudeau K;
                Length 11;
                                        Indels
                                                                                                                                                                                                                            Amyloid beta-protein fragment peptide SEQ ID NO:951.
100.0%; Score 11; DB 21; 100.0%; Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 504; 733pp; English.
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                                                                                                                                                  AAB91775 standard; Peptide; 11 AA.
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                   (first entry)
                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CONJ-) CONJUCHEM INC.
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                                                               1 GSNKGAIIGLM 11
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                         Best Local Similarity
Matches 11; Conserv
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15-OCT-1999;
                                                                                                                                                                                                  22-JUN-2001
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               Query Match
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comprising a therapeutically active amino acid region [II] and a reactive group [II] (e.g. succinimidyl and malelmido groups) attached to a less therapeutically active amino acid region [II]) and a less therapeutically active amino acid region [IV], which covalently consts therapeutically active amino acid region [IV], which covalently bends with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes.

ARBOR29 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                                  Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                             Amyloid beta-protein fragment peptide SEQ ID NO:984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 516; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milner PG,
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99US-0153406.
99US-0159783.
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(first entry)
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15-OCT-1999;
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Gaps

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Length 11; Indels

100.0%; Score 11; DB 22; 100.0%; Pred. No. 3.9e-06; iive 0; Mismatches 0;

11; Conservative

Best Local Similarity Matches 11; Conservat

Query Match

Thibaudeau K;

11

RESULT

AAW64498

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comprising a thereaft invention describes a modalised comprising a thereapeutically active amino acid region [II] and a reactive group [II] (e.g. succinimidyl and malelmido groups) attached to a less therapeutically active amino acid region [II], which covalently consists therapeutically active amino acid region [IV], which covalently beptidase stabilised therapeutic peptide composed of 3.50 amino acids. [I are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half in a specificity as bonding to large molecules decreases in the contractional prevents and interference with physiological processes. ARB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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1larity 100.0%; Pred. No. 4.8e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                         Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 507; 733pp; English
                                                                                                                                                                                                                                                                         Milner PG,
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                                                                                                                                         99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                   17-MAY-2000; 2000WO-US13576
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                             17-MAY-1999;
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15-OCT-1999;
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                                                         23-NOV-2000
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EXIX
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                                                                                                                                                                                                                             Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx; aggregate; Alzheimers disease; decoy; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates that increase calcium influx into neuronal cells. Such peptides can be used in the treatment of diseases associated with neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and orally, or from slow-release implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of aggregation of, e.g. beta-amyloid peptide - by administering decoy peptide or other calcium-influx inhibitor, useful for, e.g. treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
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                                                                                                                                                                                   Neurotoxic beta-amyloid peptide decoy peptide #11.
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                                                     AAW64498 standard; peptide; 14 AA.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                         20-0CT-1998
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-0CT-1997;
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                                                                                                                                                                                                                                                                                           Synthetic.
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AAB91782

Length 14; Indels

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(CONJ-) CONJUCHEM INC
 10-SEP-1999;
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                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                                                                 Holmes DL,
                                                                                                                                                                                     Disclosure; Page 509; 733pp; English.
                                                                                              Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB91815 standard; Peptide; 14 AA.
                              99US-0134406.
99US-0153406.
99US-0159783.
         17-MAY-2000; 2000WO-US13576.
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                                                                                                 Ezrin AM,
                                                                          (CONJ-) CONJUCHEM INC.
                                                                                                                    WPI; 2001-112059/12.
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                               17-MAY-1999;
                                         10-SEP-1999;
15-OCT-1999;
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                                                                                                                                                              Thibaudeau K;
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                                                                                                                                                              Milner PG, Holmes DL,
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                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 519; 733pp; English
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                                                                                                                                                              Ezrin AM,
                                                                                               (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                       WPI; 2001-112059/12
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10-SEP-1999;
15-OCT-1999;
                             15-OCT-1999;
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Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

WPI; 2001-112059/12.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

Disclosure; Page 515; 733pp; English.

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide components to form a peptidase stabilised therapeutic peptide components to form a reactors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. ABB90829 to AAB92441 represent invention.

Sequence 24 AA;

Gaps ; 0 Length 24; Ouery Match 100.0%; Score 11; DB 22; Length 2. Best Local Similarity 100.0%; Pred. No. 7.4e-06; Matches 11; Conservative 0; Mismatches 0; Indels

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Search completed: April 24, 2002, 09:21:50 Job time: 249 sec

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-346-849-5

US-08-346-849-5

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US-08-304-585-3

US-08-403-734-3

US-08-986-948-8

US-08-986-948-8

US-08-005-215-10

PCT-US95-10989-2

US-09-005-215-11

US-08-015-215-11

US-08-015-215-11

US-08-015-215-11

US-08-015-785-4

US-08-012-7858-36

US-08-612-7858-36

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US-08-302-808-2
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US-08-682-245A-1
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Gapop'60.0 , Gapext 60.0
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seq length: 200000000
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US-08-682-245A-2
US-08-682-245A-2
US-08-682-245A-3
US-08-682-245A-3
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## ALIGNMENTS

Gaps ; 0 GENERAL INFORMATION:

APPLICANT: Maggio, John E.

APPLICANT: Maggio, John E.

APPLICANT: Mantyh, Patrick W.

ITILE OF INVENTION: Labelled -Amyloid Peptide and Methods

TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease

NUMBER OF SEQUENCES: 3

CORRESPONDENCE SCHAPESS:

ADDRESSE: Schapegman, Lundberg & Woessner, P.A.

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN 100.0%; Score 11; DB 1; Length 11; 100.0%; Pred. No. 1.1e-05; Live 0; Mismatches 0; Indels MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,767A 600.226-US-01 Sequence 3, Application US/07744767A Patent No. 5434050 FILING DATE: 13-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUCLING, AND M.
REGISTRATION NUMBER: 33,977
REFERENCE/POCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-361 3: TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 11 amino acids Conservative TOPOLOGY: linear MOLECULE TYPE: peptide COMPUTER READABLE FORM:

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GENERAL INFORMATION:

APPLICANT: Maggio, John E.

APPLICANT: Manyh, Patrick W.

TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND

TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CURRENT APPLICATION DATA:
FILLING DATE: US/08/304,585
FILING DATE: 12-SEP-1994
                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 11; DB 1; 100.0%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMORY (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
LENGTH: 11 aming acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFRENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Mueting, Raas
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-346-849-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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COUNTRY:
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 11; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 11; Conservative 0; Mismatches 0; Indels
                                                      Sequence 2, Application US/08306872
Patent No. 5514653
GENERAL INFORMATION:
APPLICANT: Perlmutter, David H.
TITLE OF INVENTION: Method of Blocking the SEC Receptor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J Meyer, Monsanto/Searle, A3SG
                                                                                                                                                                                                                               ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MCYEL 5.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-2833
TELEPHONE: (314)694-3117
TELEPHONE: (314)694-543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08346849
Patent No. 5670483
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Two Militia Drive
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CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-306-872-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
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ZIP: 02173-4799
                   RESULT 2
US-08-306-872-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-346-849-5
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08609090
Patent No. 5840818
GENERAL INFORMATION
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: GRNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.STREET: P.O. Box 581415
CITY: Minneapolis
STATE: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 11;
  100.0%; Score 11; DB 1; Length 11; 100.0%; Pred. No. 1.1e-05; ive 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/433,734
FILING DATE: U3-MAY 1995
CLASSIFICATION: 435
ATONREY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFRENCE/POCKET UNBER: 33,977
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 11; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 3, Application US/08433734 Patent No. 5837473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 11 amino acids
Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                              1 GSNKGAIIGLM 11
                                                                                                                         1 GSNKGAIIGLM 11
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ZIP: 55458-1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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US-08-609-090-5
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US-08-433-734-3
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                                                                                              Length 11;
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Patent No. 5750349
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: BATIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                         Query Match 100.0%; Score 11; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARRE: FESTEED VERSION 1.5
CURRENT APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN 1993
FILING DATE: 25-JAN 1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV 1993
APPLICATION NUMBER: 384773/1993
FILING DATE: 16-NOV 1993
APPLICATION NUMBER: 384773/1993
FILING DATE: 16-NOV 1993
APPLICATION NUMBER: 34773/1993
RECISTRATION NUMBER: 34, 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEFAX: 200291 STRE
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 020A
ZIF: 020B
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERAING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss: single
linear
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  ; MOLECULE TYPE: peptide US-08-304-585-3
                                                                                                                                                                                                              1 GSNKGAIIGLM 11
                                                                                                                                                                                      1 GSNKGAIIGLM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-08-302-808-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 V
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                              US-08-302-808-8
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APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Bich, Alexander
APPLICANT: DiPersio, C. Wichael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATM: US/08/293,284A
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 11; DB 2; 1 100.0%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                     APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
APPLICATION NUMBER: 34,235
FRILING DATE: 28-DEC-1993
APTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELEPHONE: 617-52-3400
TELEPAX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRENEL MODEL SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08293284A Patent No. 5955343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                       FILING DATE: $25-JAN-1993 APPLICATION NUMBER: 0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexing.cu.
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSNKGAIIGLM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE:
US-08-986-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-293-284A-5
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Patent No. 595517
Patent No. 595517
Patent No. 595517
APPLICANT: SUZUKI, No. 595317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: ARTADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIKE, BRONSTEIN, ROBERTS & CUSHMAN
ADDRESSEE: LOWE PRICE LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
                                                                                                                                                                                                                                                                                                                                                                                                         434-059
                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION UNDRER: 36,190
REFERENCE/DOCKET NUMBER: 434-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DIKE, BRONSTE
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                  STREET: 99 Canal CCITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSNKGAIIGLM 11
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02019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
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US-08-986-948-8
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Gaps
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APPLICANT: Blanchard, Barbara J.
APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10989
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,872
FILING DATE: 09-SEP-1994
INFORMATION FOR SEQ ID No: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                            Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
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                                                                                  Indels
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method of Blocking the SEC Receptor NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 11; DB 5; I 100.0%; Pred. No. 1.1e-05;
                                        100.0%; Score 11; DB 4; 100.0%; Pred. No. 1.1e-05;
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/005,215 FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9510989 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09005215 Patent No. 6172043 GENERAL INFORMATION:
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                                                             Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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PCT-US95-10989-2
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                                            Query Match
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APPLICANT: Ingram, Vernon M.:
APPLICANT: Ingram, Vernon M.:
APPLICANT: Banchad, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                               Length 11;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,215
                                                                                                                                                                                                                                                                                                                             100.0%; Score 11; DB 2; I 100.0%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
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                                    REGISTRATION NUMBER: 22,592
REPERBUGE/POCKET WINDMER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFRAX: (617) 861-9540
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
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STATE: MASSACHUSETTS
COUNTRY: UNITED STATES OF AMERICA
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APPLICATION NUMBER: 60,035,847
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09005215 Patent No. 6172043
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Brook, David E.
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TELEPHONE: 617-720-3500
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REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                    LENGTH: 11 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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CLASSIFICATION:
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HYPOTHETICAL:
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GENERAL INFORMATION:
APPLICANT: Mark A. Findeis et al.
APPLICANT: Mark A. Findeis et al.
TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggre
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                   Gaps
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                                                                                                 Length 26;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 11; DB 2; L
100.0%; Pred. No. 2.5e-05;
Micmatches 0;
                                                                                                    Score 11; DB 1;
Pred. No. 2e-05;
                                                                                                                                                                   Mismatches
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FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P41,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PPI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109
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US-08-475-579A-4
; Sequence 4, Application US/08475579A
; Patent No. 5894215
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Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
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                                                                                                 100.0%;
100.0%;
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LENGTH: 34 amino acids
                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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MOLECULE TYPE:
FRAGMENT TYPE:
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         US-08-304-585-7
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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ZIP: SAABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 4;
Pred. No. 1.3e-05;
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FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08304585 Patent No. 5721106
                                                                                                                                                                                                               NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: MOE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
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US-08-304-585-7
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ITITLE OF INVENTION: LABELLED RETA-AMYLOID PERPITED AND
ITITLE OF INVENTION: MATHEMOR FOR USE IN DETECTING ALZHEIMER'S DISEASE

CORRESSEE: MUSTA
CORRESSEE: Musting, Raasch, Gebhardt & Schwappach, P.A.

STRET: PO. BOX 581415

COUNTRY: Winneapolis

COUNTRY: Wish
COUNTRY: USA
ZIP: 5445-1415

COUNTRY: USA
ZIP: 5456-1415

COUNTRY: USA
ZIP: 5456-1415

COMPUTER READABLE FORM:
MEDIUM TYEE: Plopy disk
COMPUTER: LIAM FORMATION:
SOFTWARE: PATENTAL POTAGE #1.0, Version #1.30

REPAIRE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTAL US/08/304,585

CURRENT APPLICATION NUMBER: US/08/304,585

FILING DATE: 112 - SEP-1994

CLASSIFICATION NUMBER: 33,977
RETERRING LOCACET NUMBER: 110,00010120

TELEPHONE: 612-305-127

TELEPHONE: 612-305-127

TELEPHONE: 612-305-127

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE TYPE: anino acid
STRANDENUSS: not relevant
TOPOLOGY: no
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THIS PACE BLANK USPROY

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OM protein - protein search, using sw model
                                                          Run on:
April 24, 2002, 09:23:15; Search time 38.65 Seconds (without alignments) 21.680 Million cell updates/sec
                                                                                                                                                                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: Sequence: US-09-689-469-4

Scoring table: OLIGO 11 1 GSNKGAIIGLM 11 Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size :

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries •

PIR\_68:\*

Database :

pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	. 19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر ت	4	ω	2	1	NO.	Result	
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JN0773	S31486	S31484	A39871	E86284	T10609	E70982	B82456	I52644	G82358	F72422	T22142	A30128	в83837	S63533	B83880	QRHUA4	JH0773	S00550	A27485	A49795	PQ0438	B60045	A60045	D60045	G60045	F60045	E60045	PN0512	ID		
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calponin H1 - rat	Ξ1.	H1 - pi			٠.		probable acetyltra	neuronal protein -	conserved hypothet	KHG-KDPG bifunctio	hypothetical prote	synchronous muscle	hypothetical prote		3-oxoacyl-(acyl-ca	Alzheimer's diséas	Alzheimer's diseas	S	Alzheimer's diseas	ß	Ś	Alzheimer's diseas	beta-amyloid prote	Description							

## ALIGNMENTS

Query Match 100.0%; Score 11; DB 2; Length 42; Best Local Similarity 100.0%; Pred. No. 2.5e-05; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GSNKGAIIGLM 11	RESULT 1  PN0512  beta-amyloid protein - guinea pig (fragment)  C;Species: Cavia porcellus (guinea pig)  C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999  C;Accession: PN0512  R;Shimohigashi, Y; Matsumoto, H; Takano, Y; Saito, R; Iwata, T; Kamiya, H; Ohno Biochem. Biophys. Res. Commun. 193, 624-630, 1993  A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra A;Reference number: PN0512; MUID:93290653  A;Accession: PN0512  A;Residues: 1-42 <shi> C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; amyloid</shi>
0,	H.; Ohno tein fra troteinas

RESULT

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C.Species: Ovis sp. (sheep)
C.Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995
C.Accession: E60045
R.Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A.;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d.Reference number: A60045; MUID:92017079
A.;Reference number: MRNA
A.Recession: E60045
A.;Molecule type: mRNA
A.Residues: 1-57 JOH)
A.FRESIDUES: 1-57 JOH)

A;Cross-references: EMBL:X56130 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Ωy ₽ Query Match 100.0%; Best Local Similarity 100.0%; Matches 11; Conservative 0 30 GSNKGAIIGLM 1 GSNKGAIIGLM 11 40 0; Score 11; DB 2; 1 Pred. No. 3.2e-05; Mismatches 0; Length 57; Indels 0; Gaps

0;

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Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment) c/Species: Bos primigenius taurus (cattle) C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-19: c/Accession: D60045 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid | A;Reference number: A60045; MUID:92017079 A;Accession: D60045 A;Molecule type: mRNA A;Residues: 1-57 < JOH>
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F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.;
                                                  A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease
C:Keywords: alternative splicing; A
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C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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A:Title: Conservation of the sequence of the Alzheimer's A:Reference number: A60045; MUID:92017079
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C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of t
A;Reference number: PQ0438; MUID:93075180
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R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A;Reference number: A60045; MUID:92017079
A;Accession: B60045
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A; Residues: 1-57 < JOH5
A; Cross-references: EMBL: X56125
A; Cross-references: EMBL: X56125
C; Superfamily: Alzheimer's disease amyloid beta protein; animal
C; Keywords: alternative splicing; Alzheimer's disease; amyloid;
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A;Title: Conservation of the sequence of the Alzheimer's disease amyloid A;Reference number: A60045; MUID:92017079
A;Accession: A60045
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment) C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-O
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                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision
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19-Oct-1995

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Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse N;Alternate names: proteinase nexin II C;Species: Mus musculus (house mouse) C;Dates at Mus musculus (house mouse) C;Dates at Mus musculus (house mouse) C;Accession: A27485; S19727; I49485 R;Yamada, T; Sasaki, H; Furuya, H; Miyata, T; Goto, I; Sakaki, Y. Biochem. Blophys. Res. Commun. 149, 665-671, 1987 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta prote A;Reference number: A27485; MUID:88106489 A;Accession: A27485 A;Molecule type: mRNA A;Residues: 1-695 <YAM> A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085 A;Experimental source: brain R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
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A;Title: Homology of the amyloid beta protein
A;Reference number: A49795; MUID:91273117
A;Scession: A49795
A;Stetine:
Biochim. Biophys. Acta 1129, A; Title: The amyloid beta pa A; Reference number: S19727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque C:Species: Macaca fascicularis (crab-eating macaque) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal
C;Keywords: alternative splicing; Alzheimer's disease; amyloid;
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A; Cross-references: GB:M83558; GB:M83657
R; Johnstone, E.M.; Chaney, M.O.; Norris,
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A; Molecule type: DNA
A; Residues: 1-82 <DAV>
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A; Residues: 1-695 < POD>
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A; Residues: 12-68 < JOH>
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                                           Doper, B.; van Leuven, F.; van den Berghe, H. Biophys. Acta 1129, 141-143, 1991
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7; MUID:92096458
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Gene 112, 189-195, 1992
A; Title: Positive and negative regulatory
A; Reference number: I49485; MUID:92209998
A; Accession: I49485
A; Status: translated from GB/EMBL/DDR.T
A;Experimental source: brain C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein F;625-648/Domain: transmembrane #status predicted <TMM>
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A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan A;Reference number: A41245; MUID:88264430
A;Accession: A41245
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A;Title: Alzheimer's disease amyloidogenic glycoprotein: A;Reference number: S00550; MUID:88312583
A;Accession: S00550
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C;Superfamily: Alzheimer's disease amyloid beta protein;
C;Keywords: alternative splicing; amyloid; transmembrane
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A;Accession: S19727
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-210/'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695
A;Cross-references: EMBL:X59379
A;Cross-references:
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A; Title: Purification and tissue level of
A; Reference number: A39820; MUID:91217087
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C;Date: 30-Jun-1989 #sequence_revision 30-J
C;Accession: S00550; A41245; A39820; S46251
                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 18-32 < POT>
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A; Status: preliminary
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R;Potempska, A.; Styles, J.; Mehta, P.; Kim,
J. Biol. Chem. 266, 8464-8469, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein
A;Reference number: $46251; MUID:94320627
A;Contents: annotation; copper binding sites
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A; Note: evidence for heparan sulfate attachment R; Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, FEBS Lett. 349, 109-116, 1994
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A; Residues: 1-695 <SHI>
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C;Genetics:
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A; Residues: 1-19 < RES>
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on 30-Jun-1989 #text_change 13-Aug-1999
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A; Molecule type: DNA
A; Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A; Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>
A; Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A; Note: alternative splice form APP(695)
A; Note: alternative splice form APP(695)
A; Note: alternative splice form APP(695)
B; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A; Title: Characterization of the 5'-end region and the first two exons of A; Reference number: A32277; MUID:89165870
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R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Accession: S05194
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;
4668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252
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C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993
C;Accession: JH0773
                                                                       A Molecule type: DNA
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A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded A; Reference number: S02260; MUID:89128427
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C; Species: Homo sapiens (
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A; Residues: 1-288,'V',365-770 <LEM1>
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A; Residues: 1-747 <OKA>
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                                         Cross-references:
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11; Conserv
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   Chaney,
   GB:M24546; GB:M24547; NID:g341202; PII
Chaney, M.O.; Moore, R.E.; Ward, K.E.;
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Pred. No.
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   PIDN:AAC13654.1;
E.; Norris, F.H.;
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   PID:g516074
Little, S.P.
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A; Note:
R; Kang,
Nature 3
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R; Levy, 1
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A; Residues: 672-710 < PRE1>
A; Note: 693-Gln was found
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A; Residues: 687-718 < KAM2>
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A; Residues: 687-692, 'G',
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A; Residues: 1-770 < YOS1>
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ion: B44017
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V

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A; Status ......
A; Molecule type: DNA
A; Residues: 656-737 <LEV>
A; Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.
A; Note: a mutation with 693-Gln is presented
A; Note: a mutation with 693-Gln is presented
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A;Title: Linkage and mutational analysis of familial Alzheime A;Reference number: A44017; MUID:93035397
A;A;Accession: A44017
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A; Title: A mutation in the amyloid precursor A; Reference number: I59562; MUID: 92022553
A; Accession: I59562
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A;Reference number: A59020, MUID:91340168
A;Contents: annotation; erratum
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A; Residues: 1-530, 'QWLMPVIPAFWEAKVGR' < YOS2>
A; Cross-references: GB: M34875; NID: g178608; PIDN: AAB59501.1; PID: g178615
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Gene 87, 257-263, 1990
A;Title: Genomic organization of the human
A;Reference number: I39451; MUID:90236318
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A;Accession: A35486
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A;Title: Expression of a normal and variant Alzheimer's beta-protein generative.
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                                                                                        A; Experimental source: familial Alzheimer disease family A; Note: sequence extracted from NCBI backbone (NCBIP:115
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; A;Experimental source: familial Alzheimer disease family SB
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                                                                                                                                                A; Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1;
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sequence extracted from NCBI backbone (NCBIP:115376) this sequence has a silent mutation J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Mast 325, 733-736, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          revised physical map for reference E.; Carman, M.D.; Fernandez-Madrid,
                                                                                                                                                                                                                                                                                                                                                     ,694-718 <KAM1>
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M.E.; Pulst, S.
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R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein A;Reference number: $00707; MUID:88122640
A;Accession: $00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:x06982; NID:928817; PIDN:CAA30042.1; PID A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhift P. -----
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A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; Pl
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; E
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNJ
A;Reference number: A47585; MUID:87120329
A;Accession: A47585
                                A; Title: Novel precursor of Alzheimer's disease amyloid prot A; Reference number: A38949; MUID:88122641
A; Accession: A38949
A; Molecule type: mRNA
A; Residues: 287-367 < KIT>
A; Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1;
A; Experimental source: glioblastoma cell line
A; Experimental source: glioblastoma PP(770)
R; Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Ba Brain Res. Mol. Brain Res. 4, 121-131, 1988
A; Title: Absence of mutation in the beta-amyloid cDNAs clone
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A:Title: A new A4 amyloid mRNA contains a domain homolog A; Reference number: S00925; MUID:88122639
A; Accession: S00925
A; Accession: S00925
A; MUID:88122639
A; MUID:8812639
A; MUID:88122639
A; MUID:8
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A; Residues: 674-703 <TAN1>
A; Cross-references: GB:M15532; NID:g177957; PIDN:AA
R; Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum,
EMBO J. 7, 949-957, 1988
A; Title: Identification, transmembrane orientation
A; Reference number: S02638; MUID:88296437
A; Accession: S02638
Brain Res. Mol. I
A;Title: Absence
A;Reference numbe
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A;Title: Characterization and chromosomal localization A;Reference number: A47584; MUID:87120328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.; Gonzalez-DeWhitt, P.; Schilling, 31, 525-527, 1988
                                             beta-amyloid cDNAs cloned from
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albaum, J.M.; Lema
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A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573 A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC B as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT A;Note: the cited Genbank accession number, J03594, is not in release 101 R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.;
                                                                                                                                                                                                                                                                                    R:Zain, S.B.; Sallm, M.; Chou, W.G.; Sajdel-Sulkowska, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988 A;Title: Molecular cloning of amyloid cDNA derived from A;Reference number: A31087; MUID:88124954 A;Accession: A31087
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A; Residues: 122-288, 'V', 365-770
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A; Residues: 507-770 <ZAI>
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A;Gene: BH1842 C;Superfamily: ribitol dehydrogenase; C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 A;Cross-references: GB:AP001513; GB:BA000004; A;Experimental source: strain C-125 A; Reference number: A; Accession: B83880 R; Takami, H.; Nakasone, K.; Takaki, Y.; Nucleic Acids Res. 28, 4317-4331, 2000 R;Takami, H.; A; Residues: A; Status: preliminary A; Title: Complete genome C; Accession: B83880 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [imported] -A; Molecule type: DNA ;Genetics: BH1842 1-247 <STO> enome sequence of the alkaliphilic bacterium A83650; MUID:20263314 short-chain Maeno, NID:g10174345; ດ : alcohol #text\_change 31-Dec-2000 Sasaki, dehydrogenase R.; PIDN:BAB05561.1; GSPDB:G Bacillus halodurans Masui, Bacillus halodurans . . homology

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profilin basic isoform - Entamoeba hist C;Species: Entamoeba histolytica C;Date: 28-oct-1996 #sequence\_revision C;Accession: S63533; S63474 R;Binder, M.; Orther, S.; Erben, H.; Sc Eur. J. Biochem. 233, 976-981, 1995 A;Title: The basic isoform of profilin RESULT Entamoeba histolytica Scheiner, O.; 13-Mar-1997 Wiedermann, #text\_change G.; 26-Aug-1999 Valenta,

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A;Réference number: $63474; MUID:96085166
A;Accession: $63533
A;Molecule type: mRNA
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A;Cross-references: EMBL:X90911; NID:91070154; PID:91070155
A;Accession: $63474
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C;Superfamily: profilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnstone E.M., Chaney M.O., Norris F.H., Pascual "Conservation of the sequence of the Alzheimer's peptide in dog, polar bear and five other mammals polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH INTRACELLULAR SIGNALING PATHWAY THROUGH THE G
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae;
  PROTEIN
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SUBCELLULAR LOCATION: TYPE I MEMBRANE
SIMILARITY: BELONGS TO THE APP FAMILY.
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s requires a license agreement (See
an email to license@isb-sib.ch).
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(Rel. 35, Last sequence update)
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DISEASE AMYLOID A4 PROTEIN HOMOLOG
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                       DISEASE
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SE AMYLOID A4 PROTEIN HOMOLOG
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  (A-BETA)] (FRAGMENT).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                     [CONTAINS:
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                     BETA-AMYLOID
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ALZHEIMER'S
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Q28748;
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SEQUENCE
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between
MEDLINE-92017079; PubMed-1656157; Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
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PROSITE; F
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HSSP;
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Brain Res. 10:299-305(1991).
1- FUNCTION BRAIN RES. 10:299-305(1991).
1- FUNCTION FUNCTIONAL BURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING
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                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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NON_TER
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modified and
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Mammalia; Eutheria;
                                                              TISSUE=Brain;
                                                                                                  NCBI_TaxID=9986;
                                                                                                                                        Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
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                                                                            SEQUENCE
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SUBCELLULAR LOCATION: TYPE I MEMBRANE SIMILARITY: BELONGS TO THE APP FAMILY.
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P05067; 1AML.
                                                                                                                                                                (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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PS00319; A4_EXTRA; PARTIAL.
PS00320; A4_INTRA; PARTIAL.
tein; Amyloid; Neurone; Tran
                                                                         FROM N.A.
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7 AA;
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DISEASE AMYLOID A4 PROTEIN HOMOLOG
                                                                                                                                        cuniculus
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                                                                                                                                                                                                                                          STANDARD;
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                                                                                                   Js (Rabbit).
Chordata; Craniata; Ver
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58
58
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Carnivora; Fissipedia;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                    Score 11;
Pred. No.
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                                                                                                                                                                                                                                          58
                                                                                                                           Vertebrata;
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ia; Canidae;
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                                                                                                               Oryctolagus
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                                                                                                                                                                             [CONTAINS: BETA-AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                 Length 58
                                                                                                                           Euteleostomi;
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Canis.
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Best Local S
Matches 11
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Q28757;
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01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                              MEDLINE=92017079; pubMed=1656157;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little "Conservation of the sequence of the Alzheimer's disease amyl peptide in dog, polar bear and five other mammals by cross-sp polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).

-i- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING FUNCTIONAL NEURONAL NEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Caprinae;
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
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NON_TER
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PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                 G(O) (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE
SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH
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Cetartiodactyla; Ruminantia;
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Pred. No. 1.3
); Mismatches
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                   I MEMBRANE
APP FAMILY.
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
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minantia; Pecora; Bovoidea
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THE GTP-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 58;
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amyloid
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SO SECTION OF SECTION 
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SEQUENCE
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-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH CONTRACTOR OF THE RESERVANCE OF T
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE ANYLOID A4 PROTEIN HOMOLOG (CONTAINS: BETA-AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Tran
InterPro; IPR001868; A4_APP.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Tran
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                                                                                                                HSSP;
                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                   modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnstone E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92017079; PubMed=1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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X56126; CAA39591.1;
P05067; LAML.
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                                                                                                                                                                                                                          equires a license agreement (semail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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Q95241;
15-DEC-1998
15-DEC-1998
15-DEC-1998
20-AUG-2001
ALZHEIMER'S
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CHAIN
DOMAIN
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SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
PROSITE; PS000319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1;
                                                                                                                                                                                                                                                                                                                                            + +
                                                                                                                                                                                                                                                                                                                                                                             Levy E., Amorim A., Frangione B., Walker L.C.;
"Beta-amyloid precursor protein gene in squirrel
cerebral amyloid angiopathy.";
Neurobiol. Aging 16:805-808(1995).
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH
INTRACELLULAR SIGNALING PATHWAY THROUGH THE G
                                                             PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
                                                                                                   Pfam;
                                                                                                                       InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                 EMBL; S81024; AAD14347.1;
                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Liver, and Kidney;
MEDLINE-96108492; PubMed-8532114;
Levy E., Amorim A., Frangione B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Mammalia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saimiri sciureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSNKGAIIGLM
                                                                                                                                                                                                                                                                                                     SÜBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
MPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
                                                                                                                                                                                                       ween the Swiss Institute of Bioinformatics and the I
European Bioinformatics Institute. There are no resi
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDE PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSNKGAIIGLM
                                                                                                 PF02177; A4_EXTRA; 1. PF00014; Kunitz_BPTI; 1.
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
DISEASE AMYLOID A4 PROTEIN PRECURSOR (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Common squirrel monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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EXTRACELLULAR (POTENTIAL
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Ven
Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ni; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                             squirrel monkeys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                 http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                              Usage
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Cebinae; Saim
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RESULT
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Best Local
Matches 1
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DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal;
SIGNAL
CHAIN
                                  Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Unterbeck A., Beyreuther K., Mueller-Hill B.; "The PreA4(695) precursor protein of Alzheimer's is encoded by 16 exons."; Nucleic Acids Res. 17:517-522(1989).
                                                                                                                                                                                          MEDLINE-87144572; PubMed=2881207; Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B. "The precursor of Alzheimer's disease amyloid A4 protein rescell-surface receptor."; Nature 325:733-736(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DOMAIN
                                                                                                   proteinase inhibitors.";
Nature 331:525-527(1988)
[3]
                                                                                                                                            MEDLINE=88122639; PubMed=2893289;
Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller
Greenberg B., Davis K., Wallace W., Lieberburg I., F
                                                                                                                                                                                      Nature
[2]
                  SEQUENCE
                                                                                SEQUENCE FROM N.A. MEDLINE=89128427; PubMed=2783775;
                                                                                                                     Cordell B.;
"A new A4 amyloid mRNA contains a
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
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Hattori M.,
        MEDLINE-97263807;
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11; Conserv
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552
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         PubMed=9108164;
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BY SIMILARITY.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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Pred. No. 9.7
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CYTOPLASMIC
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A4 PROTEIN
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9.7e-05;
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                                                      disease
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Fuller
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                                                      A4
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Tsukahara

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Furuhata

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encodes
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[5]
           Sinha
"The s
                     MEDLINE-89384866; PubMed=2506449;
Oltersdorf T., Fritz L.C., Schenk
Johnson-Wood K.L., Beattie E.C., V
Sinha S.;
                                                                                                                                                                                                                                                                             gene.
                                                                                                                                                                                                                                                                                                                                                                         Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Tourtellotte W.W., Huebner V., Shively J.E.; "Amyloid angiopathy of Alzheimer's disease: amino aci and partial sequence of a 4 200-3-1---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease brain: coding mRNA are expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and characterization of a cDNA encoding cerebrovascular and the neuritic plaque amyloid peptides." Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitaguchi N., Takahashi Y., Tokushima Y
"Novel precursor of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing of
Nucleic Acids
                                                                                                                                                                                                      MEDLINE=89016647; PubMed=3140222; Schon E.A., Mita S., Sadlock J.,
                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                     MEDLINE=90236318; PubMed=2110105;
Yoshikai S.-I., Sasaki H., Doh-Ur
                                                                                                                                                                                                                                                                                                                                                               microvessels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protease inhibitor domain enco
mRNA associated with Alzheimer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88122640; PubMeTanzi R.E., McClatchey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
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331:530-532(1988).
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                                                                                                                                                                 .A., Mita S., Sadlock J., Herb
specifying the human amyloid
a 95-kDa polypeptide.",
Acids Res. 16:9351-9351(1988)
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STRUCTURE BY NMR OF 6/2-02.
STRUCTURE 94281210; PubMed=7516706;
MEDLINE=94281210; PubMed=7516706;
Talafous J., Marchowski K.J., Klopman
"Solution structure of residues 1-28 of
Riochemistry 33:7788-7796(1994).
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[14]
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Poulsen S.-A., Wat
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Tamburini P.P.;
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"Crystal structure
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                                                                                                B359783; PubMed=9693002;
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                                                               PubMed=10940222;
tson A.A., Craik
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noto T., Matsuura
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[24]
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                                                                                                                                                                 MEDLINE=89345111; PubMed=2569710; Fukuchi K., Martin G.M., Deeb S.S.; "Sequence of the protease inhibitor di precursor of Mus domesticus."; Nucleic Acids Res. 17:5396-5396(1989)
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Mammalia; Eutheria;
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01-DEC-1992 (Rel. 24, Last seguence update)
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ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
(AMYLOIDOGENIC GLYCOPROTEIN) (AG).
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Science 256:780-783(1992).
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Yamada T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-289 AND
                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada T., Sasaki H., Furuya H., "Complementary DNA for the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88106489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Strooper B., van Leuven F., van den Berghe H.;
"The amyloid beta protein precursor or proteinase
is closer related to its human homolog than previ
Biochim. Biophys. Acta 1129:141-143(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92096458; PubMed=1756177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92271194;
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                                                                                 9 FROM N.A.
98; PubMed=1555768;
Yoshikai S.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3322280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND 365-770 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed-1589757;
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Rodentia;
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EMBL; X59379; -; NOT_ANNOTATED_CDS.
EMBL; M18373; AAA37139.1; -.
EMBL; X15210; CAA33280.1; -.
EMBL; D10603; BAA01456.1; -.
EMBL; D10603; BAA01456.1; -.
EMBL; M24397; AAA39929.1; -.
PIR; A27485; A27485.
PIR; S04855; S04855.
PIR; S19727; S19727.
                                                                                                                                                                                   DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1;
PROSITE; PS50279; BPTI_KUNITZ_2;
Glycoprotein; Amyloid; Neurone; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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i. SUBCELLULAR LOCATION: TYPE
i. ALTERNATIVE PRODUCTS: 5 ISC
APP(751) AND APP(770) (SHO
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the succession of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 281-380 FROM N.A., TISSUE-Brain, and Kidney; MEDLINE-89149813; PubMed=24932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
"Structure and expression of the alternatively-spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOC
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLICING.
TISSUE SPECIFICITY: AAA(770) 1
WIDELY EXPRESSED. AAA(695) IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF02177; A4_EXTRA; 1. PF00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00006;
SM00131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunitz_BPTI.
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                                                                                                                                                                                                                                                                                                                                                                                      Neurone; Transmembrane;
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5 ISO
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                    BPTI/KUNITZ INHIBITOR.

CLATHRIN-BINDING (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF CLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

E -> V (IN ISOFORM APP(695)).

MISSING (IN ISOFORM APP(751)).
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EQUIVALENT OF BETA-AMYL
                                                                                                                                                                                                                                                                EXTRACELLULAR POTENTIAL.
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BY SIMILARITY.
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S EXPRESSED IN BRAIN, KIDNEY AND
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APP(395), APP(563), APP(695),
); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions
                                                                                                                                                                                                                                                                                                                         DISEASE AMYLOID
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Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A4_RAT
P08592;
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatified and this statement is not removed. Usage by and formatified and this statement is not removed.
             PRINTS; PRO0203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
                                                                                                              PIR;
                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AuG-1988 (Rel. 08, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
                                                  InterPro; IPR001868; A4_APP.
InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
                                                                                                                                     EMBL; X07648; CAA30488.1; -. EMBL; X14066; CAA32229.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=88312583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89183625; PubMed=2648331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 289-364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-289 AND 365-770 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alzheimer's disease amyloidogenic
in rat brain suggests a role in cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     696
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                                                                                                                                                                                                                                                                                    WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

SIMILARITY: BELONGS TO THE APP FAMILY.

SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563),
APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY A
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: THE CLATHRIN-BINDING SITE
                                                                                                                                                                                                                                                                                                                                                                                           SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                               J., Mueller-Hill B.;
sequence of the two extra exons in rat preA4.";
eic Acids Res. 17:2130-2130(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSNKGAIIGLM
                                                                                                             $00550; $00550.
$03607; $03607.
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7:1365-1370(1988).
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A4_EXTRA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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   cell contact.";
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                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                 outstation
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Best Local
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SEQUENCE
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     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. They use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPT_KUNITZ 1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing; Serine protease inhibitor SIGNAL 1 17 By SIMILARITY.
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                              cDNA cloning, heterologous properties.";
                                                                                                                                                                                                                                                                                                 Eukaryota; Entamoebidae;
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                      ENTHI
                                                                                                ÷
                                                                                                                                                                                                                    Valenta R., Duchene M.; "The basic isoform of profilin in pathogenic Entamoeba
                                                                                                                                                                                                                                         MEDLINE=96085166; PubMed=8521867; Binder M., Ortner S., Erben H., Scheiner
                                                                                                                                                                                                                                                                   STRAIN=SFL-3
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                696 GSNKGATIGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GSNKGAIIGLM
                                                                                                                             . J. Biochem. 233:976-981(1995).

FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE CYTOSKELETON, AT HIGH CONCENTRATIONS, PROFILIN PREVENTS POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORM IP3 AND DG.
                                                                                             ACTIN IN A 1:1 RATIO
SIMILARITY: BELONGS
                                                                                                                    SUBUNIT:
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MISSING (IN ISOFORM APP(695)).
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BY SIMILARITY.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                  (See http://www.isb-sib.ch/announce/
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                              Usage
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                                                                                                                    COMPLEX WITH MONOMERIC
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                                                                                                                                                                RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RN Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RN George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RN Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RN Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RN Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RN Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RN Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RN Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RN Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RN Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RN Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RN Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RN Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RN Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RN Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RN Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RN Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RN Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RN Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,
RN Glodek A., Gong F., Go
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HSSP; P07274; 1YPR.
InterPro; IPR002097; Profilin.
Pfam; PF00235; profilin; 1.
SMART; SM00392; PROF; 1.
PROSITE; PS00414; PROFILIN; 1.
Actin-binding; Cytoskeleton.
SEQUENCE 130 AA; 13237 MW; F
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P1431B; Q9V6M7;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MUSCLE-SPECIFIC PROTEIN 20.
MP20 OR TPN OR CG4696.
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nixon K.A., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ayme-Southgate A., Lasko P., French C., Pardue M.L.; "Characterization of the gene for mp20: a Drosophila that is not found in asynchronous oscillatory flight J. Cell Biol. 108:521-531(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CANTON-S; TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
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InterPro; IPR003247; CH_type
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Pfam; PF00402; Calponin; 1.
Pfam; PF00307; CH; 1.
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NEURONAL PROTEIN !
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                                   "Mouse neuronal protein
Submitted (AUG-1999) to
-i- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                      MOUSE
                                                                                     SEQUENCE FROM
                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                        Hayashi A.,
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L. 40, Last sequ
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Rodentia;
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                                  Okaze H., Kozuma S., Sel
(NP25).";
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TO THE CALPONIN FAMILY.
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InterPro; IPR003247; CH_type.
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InterPro; IPR003096; SM22_calponin.
           EMBL; M84725; AAC42095.1; -.
InterPro; IPR003247; CH_type.
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
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PRINTS; PR00890; TRANSGELIN.
Probom; PD001527; CH_type; 1.
SMART; SM00033; CH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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PRINTS; PR00888; SN22CALPONIN.
PRINTS; PR00880; TRANSGELIN.
PRODOM; PD001527; CH_type; 1.
SMART; SM00033; CH; 1.
PROSITE; PS01052; CALPONIN; 1.
PROSITE; PS01052; CALPONIN; 1.
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Swee http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            Platzer J., Schmitt R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M) MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS FLGG IN THE DISTAL PORTION, AND FLGB, FLGC AND FLGF ARE THOUGHT BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS EACH (BY SIMILARITY).
                                                                                                                  Flagella.
SEQUENCE
                                                                                                                                         EMBL; L49337; AAB81413.1; -.
InterPro; IPRO01444; Flag_bb_rod.
Pfam; PF00460; flg_bb_rod; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FLAGELLAR BASAL-BODY ROD PROTEIN FLGG (DISTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q52946;
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Beta-amyloid pepti Beta-amyloid pepti Beta-amyloid pepti Beta-myloid pepti Amyloid beta-prote Amyloid beta-prote Synthetic amyloid Beta-amyloid (1-38 Human tachykinin a Amyloid beta-prote Amyloid beta-prote Beta-amyloid (1-39 Human myloid beta Synthetic amyloid Human Receptor to Beta-amyloid pepti Beta-amyloid beta prote Amyloid beta pepti Beta-amyloid pepti	0.0.00

### ALIGNMENTS

RESULT AAR60369

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AAR60369 standard;

peptide;

11 AA.

Beta-amyloid (25-35).

15-MAR-1995 AAR60369;

(first entry)

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05-FEB-1993;
16-NOV-1993;
28-DEC-1993;
Antibodies recognising specific parts of beta-amyloid - used for diagnosis of diseases implicating beta-amyloid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope
                                                                                                                                                                                                              WPI; 1994-264110/32.
                                                                                                                                                                                                                                                                                                                                         Kitada
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93JP-0334773.
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Matches 11
                                                                                                                                                                                                                           Claim
                                                                                The invention relates to new chemical compounds which are peptides of formulae XXXX (I), XXNXZ (II) and XINXXX (III), and peptides comprising the sequences (I), (II) or (III) and containing not greater than 8 amino acid residues. In the formulae, X is any amino acid with a cationic side chain, N and Z are neutral amino acids, and two of X1, X2 and X3 are amino acids with an anionic side chain and the third is an amino acid with an anionic or neutral side chain and the third is an amino acid with an anionic or neutral side chain. Also new is the peptide Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is the latter undecapeptide which represents amino acids 25-35 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's
                                         beta-amyloid peptide A-beta.
The peptides inhibit the binding of glycosaminoglycans and/or proteoglycans to A-beta peptide and hence can be used for preventing the
                                                                                                                                                                                                                                                                    Treating Alzheimer's disease by using cpds.
                                                                                                                                                                                                                                                                                                 WPI;
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                           of amyloid
                                                                                                                                                                                                                           Page 64;
  11
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    to glycosaminoglycan(s)

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                            for treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plaque; glycosaminoglycan;
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Amyloid beta peptide

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                                                                                                                                                                                                                                                          Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor - used for inhibiting amyloid-beta protein neurotoxicity in e.g. Alzheimer's disease
                         12-MAR-1998
                                          AAW23336
                                                          AAW23336
                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's
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                                                                                                                                       Conservative
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                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 95WO-US10989
                                                                                                                                                                                                                                                                                                                                                                                                                                 96; beta-amyloid; treatment; Alzheimer's disease; inhibition; neurotoxicity; beta-amyloid 25-35.
                                                          peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                           English.
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Pred.
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                                                                                                                                       Mismatches
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                                                                                                                                               0.00034;
                                                                                                                                                        DB 17;
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                                                                                                                                                      Length 11;
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                                                                                                                                       Indels
                                                                                                                                                                                                          and Down's
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                                                                                                                                      Gaps
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RESULT
AAW64497
ID AAW6
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AC AAW6
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AC AAW6
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DT 20-C
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DE Neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC is the principal component of extracellular deposits in Alzheimer's CC disease. It has been shown to promote nuerite outgrowth, generate CC reactive oxygen intermediates, induce cellular oxidant stress, lead to CC neuronal cytotoxcity, and promote microglial activation. The present CC peptide, which comprises amino acids: 25-35 of the amyloid beta peptide, cc is used in a pharmaceutical composition. This composition comprises an agent capable of inhibiting interaction of an amyloid beta peptide with CC a receptor for advanced glycosylation end product and a carrier. A CC method for inhibiting interaction of amyloid beta peptide with CC a receptor for advanced glycosylation end product and a carrier. A CC thibiting the interaction between the amyloid beta peptide with a receptor for advanced glycosylation can be used for inhibiting CC thibiting the interaction between the amyloid beta peptide and the creceptor for advanced glycosylation can be used for inhibiting CC degeneration of a neuronal cell, inhibiting aggregation of an amyloid beta peptide fibril on a cell, inhibiting aggregation of amyloid beta peptide fibril on a cell, inhibiting aggregation of amyloid beta peptide on the surface of a cell, inhibiting affiltration of a microglial cell by amyloid beta peptide. The methods can be used for treating e.g. CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic catherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia amylotion of amyloid beta peptide. The methods can be deed contraction of amyloid beta peptide. The methods can be deed contraction dementia amylotomy syndrome, dementia contraction syndrome syndrome syndrome.
                                                                                                                                                                                                                                                                                         δÃ
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent which inhibits interaction of an amyloid-beta peptide with a receptor for advanced glycosylation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAW23335-36 are portions of the the amyloid beta peptide, which is the principal component of extracellular deposits in Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-393374/36.
Neurotoxic beta-amyloid peptide decoy peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis, neuronal cytotoxicity, Down's sy associated with head trauma, amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5;
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                                              20-OCT-1998
                                                                                           AAW64497;
                                                                                                                                     AAW64497
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                                                                                                                                                                                                                                                                         GSNKGAIIGLM 11
                                                                                                                                                                                                                                                  gsnkgaiiglm 11
                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or neuronal degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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                                            (first entry)
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                                                                                                                                 peptide;
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                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 18;
Pred. No. 0.00034;
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                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sclerosis, multiple
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AAW47231
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates that increase calcium influx into neuronal cells. Such peptides can be used in the treatment of diseases associated with neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and orally, or from slow-release implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibition of aggregation of, e.g. beta-amyloid peptide - by administering decoy peptide or other calcium-influx inhibitor useful for, e.g. treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-amyloid peptide;
aggregate; Alzheimers
                                                                                                                                                                                                                                               AAW47231 standard; peptide; 11 AA.
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(MINU ) HARVARD COLLEGE.
                                                                                                        US5721106-A.
                                                                                                                                                  amyloidosis
                                                                                                                                                                                Beta-amyloid peptide residues
                                                                                                                                                                                                       22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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10-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggregate;
                                12-SEP-1994;
13-AUG-1991;
                                                               12-SEP-1994;
                                                                                     24-FEB-1998
                                                                                                                             Homo sapieńs
                                                                                                                                                            Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 42;
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                                                                                                                                                            assay;
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                                                                                                                                            σσαγ; σετα-amyloid peptide; treatment;
disease; Alzheimer's disease.
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                                                                                                                                                                                                       (first entry)
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                                94US-0304585
91US-0744767
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97US-0035847
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                                                              94US-0304585
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                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-AP; neuropeptide; neurotoxin;
disease; decoy; treatment.
                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                 25-35.
                                                                                                                                                                                                                                                                                                                                               Mismatches
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0.00034;
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AAW81470
ID AAW8
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Best Local
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       Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence was used in the development of a novel in vitro screening assay for agents capable of affecting the deposition of beta-amyloid peptide (BAP) on tissue. The method comprises contacting a silk sample with labelled BAP, optionally in the presence of a test agent, detecting the amount of label bound to the silk and assessing the effect of the agent on the deposition of BAP. Agents that inhibit binding of BAP to silk are potentially useful for treating amyloidosis diseases, especially Alzheimer's disease.
                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                   Synthetic amyloid beta (Abeta)
                                                                                                                                                                                                                                                                                                                                                                               AAW81470;
  acetonitrile
                                                                                                                                                                       (KENT)
                                                                                                                                                                                            29-FEB-1996;
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                                                                                                                                                                                                                                                           US5840838-A
                                                                                                                                                                                                                                                                                                   research;
                                                                                                                                                                                                                                                                                                                Amyloid
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                                                                                                                                                                                                                                                                                                                                                                                                    AAW81470 standard;
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                                                                                                                               1999-034120/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vitro screening assay for Alzheimer's disease ses assessing binding of labelled beta-amyloid
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                                                                                                                                                                        VIND
                                                                                                                                                                                                                                                                                                                beta;
                                                                                             for treating synthetic treatment, useful for s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                        Columns 9-10;
                                                                                                                                                                                                                                                                                                    neurotoxicity;
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                                                                                                                                                                                                                                                                                                                Abeta;
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                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
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                                                                                                                                                                                                                                                                                                               deoxygenated solvent;
                                                                       14pp;
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                                                                                                                                                                                                                                                                                                   free-radical;
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Pred.
                                                                                             studying
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                                                                                                                                                                                                                                                                                                   glutamine synthetase
                                                                                                         beta
                                                                                             beta peptides neurotoxicity
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                                                                                                                                                  Hensley
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mg/ml,
                                                                                                                                                                                                                                                                                                               evaporative deposition;
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peptide to silk
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Sequence

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Best Local S
Matches 11
                                  This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in
                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                            Inhibiting
                                                                                                                                                                                                                                                                                                                                                                            (UYCO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invasion;
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| gsnkgaiiglm 11
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11; Conserv
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                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                  Page 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis;
                                                                                                                                                                                                                                                                            tumour invasion or spreading by administration or advanced glycation endproducts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 advanced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RAGE)
                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generating capacity and glutamine
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycation endproducts;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment #2
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                                                                                                                                                                                                                                                                                            of soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour;
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8 В

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RESULT
AAB91775
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Best Local (
           Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                       peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from pendes activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                       The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a period of the contractive amino acid region (IV).
                                                                                         intracellular uptake and interference with physiological process: AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 504; 733pp;
                                                                                                                                                                                                                                                                                                                                                                                   Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONJ-) CONJUCHEM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protection; endogenous therapeutic peptide; peptidase; conblood component; modification; succinimidyl; maleimido grohydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>_</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP,
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            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                  AA;
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99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide; 11
           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milner
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                                                                                                                                                                                                                                                                                                                                           English
         Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
0.00034;
            0.00034;
                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidase; conjuga
; maleimido group;
                                                                                                                                                                                                                                                                                                                                                                                   to albumin prevents length of in vivo ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                        Length 11;
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Indels
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0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino;
                                                                                                                                                                                                                                                                                                                                                                                   activity
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                                                                                                                                                                                                                               growth
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0,
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ID AABS
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                                                      Matches
                                                                 Query Match
Best Local :
                                                                                                                   Sequence
           1 GSNKGAIIGLM 11
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Gaps

gsnkgaiiglm

Similarity 11; Conser

100. ilarity 100. Conservative

.0%;

Score 54; DB 22; Pred. No. 0.00034;

Length Indels

11

0;

Gaps

0;

0;

Mismatches

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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases and suggestificity as bonding to large molecules decreases. AAB90829 to AAB9241 represent peptides which can be used in the ceeping the period of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modifying and attaching therapeutic peptidase degradation, useful for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2000; 2000WO-US13576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amyloid beta-protein fragment peptide SEQ ID NO:984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CONJ-) CONJUCHEM INC
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||||||||||
1 gsnkgaiiglm :
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11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 516; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
AA;
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99US-0153406.
99US-0159783.
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RESULT 11
AAW64498
ID AAW644
XX AAW644
XX AW644
XX Beta-a
KW Beta-a
CC AAW644
CC AAW644
CC AAW644
CC Deptic
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AAB91782
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Best Local 9
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                                                            Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARM64488-W64517 are decoy peptides that bind to a neurotoxic beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to form aggregates that increase calcium influx into neuronal cells. Such peptides can be used in the treatment of diseases associated with neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by injection and orally, or from slow-release implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibition of aggregation of, e.g. beta-amyloid peptide - by administering decoy peptide or other calcium-influx inhibitor, useful for, e.g. treating Alzheimer's disease
Synthetic
                                                                                                                                           22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-398795/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1997;
10-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-amyloid
                                                                                                          Amyloid
                                                                                                                                                                          AAB91782;
                                                                                                                                                                                                        AAB91782 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurotoxic beta-amyloid peptide decoy peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1998
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                                                                                                                                                                                                                                                                                                     1 GSNKGAIIGLM 11
                                                                                                                                                                                                                                                                                   4 gsnkgaiiglm
                                                           component;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                          beta-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     id peptide; beta-AP;
Alzheimers disease;
                                                                                                                                                                                                                                                                                                                                                                                                                               14 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ingram
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97US-0035847.
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                                             hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68pp; English.
                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                         fragment peptide
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                                            growth
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Pred. No.
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decoy; treatment.
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                             factor;
                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                  0.00044;
                                          neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                            IJ
                                                                                                            NO:958
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Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino

hormone;

growth factor;

neurotransmitter.

Amyloid beta-protein fragment peptide SEQ ID NO:964.

22-JUN-2001 AAB91788; AAB91788

(first entry)

Synthetic WO200069900-A2

Homo sapiens hydroxyl; thiol; AAB91788 RESULT

standard;

Peptide;

14

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                                                                                                                                                                 The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to CC a less therapeutically active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids. CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic compises are not suitable as drug candidates as they require frequent cadministration due to rapid degradation by peptidases in the body. CC modifying and attaching therapeutic peptides to albumin prevents or CC reduces the action of peptidases to increase length of activity (half CC life) and specificity as bonding to large molecules decreases CC intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CX CX exemplification of the present invention.
                                                       Query Match
Best Local Similarity
Matches 11; Conserv
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10-SEP-1999;
15-OCT-1999;
                                                                                                                                           Sequence
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4 gsnkgaiiglm
                              1 GSNKGAIIGLM
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                                                                Conservative
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   733pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y therapeutic peptides useful for increasing
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Pred. No. 0.00044;
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                                                                Mismatches
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RESULT
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17-MAY-1999;
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                                                                                                        Synthetic
                                                                                                                                                          Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino.
                                                                                                                                                                                                    Amyloid beta-protein fragment peptide SEQ ID
                                                                                                                                                                                                                                                          AAB91815;
                                                                                                                                                                                                                                                                                    AAB91815 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intracellular uptake and interference with physiological AAB90829 to AAB92441 represent peptides which can be used
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                                                                                                                     Homo sapiens
                                                                                                                                               hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                     DP,
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ll; Conservative
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-+ive 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                         0.00044;
hes 0;
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length of i
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AAB91805
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(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.

ABB90829 to ABB92441 represent peptides which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                    17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                    99US-0134406.
99US-0153406.
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Pred. No. 0.00044;
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(CONJ-) CONJUCHEM INC

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The present invention describes a modified therapeutic peptide (I)
C comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not sultable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB9241 represent peptides which can be used in the
CC exemplification of the present invention.
Sequence
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          24 AA;
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Search completed: April 24, 2002, 09:17:36 Job time: 140 sec 밁 Ş Ouery Match 100.0%; Score 54; DB 22; Best Local Similarity 100.0%; Pred. No. 0.00078; Matches 11; Conservative 0; Mismatches 0; Length 24; Indels 0; Gaps

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Minimum
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Listing first 45 summaries
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/
2: //gn2_6/ptodata/2/
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4: //gn2_6/ptodata/2/
5: //gn2_6/ptodata/2/
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
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US-08-346-849-5
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US-08-303-3734-3
US-08-433-734-3
US-08-609-990-5
US-09-905-215-10
US-09-905-215-11
US-08-915-793A-4
US-08-612-785B-16
US-08-612-785B-36
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US-08-612-785B-36
US-08-612-785B-40
US-08-302-808-1
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Query Match
Best Local Similarity
Matches 11; Conserv

Conservative

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Score 54; DB 1; Pred. No. 0.00035; Mismatches 0;

Length 11; Indels

0;

Gaps

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RESULT 1 US-07-744-767, Sequence 3, Patent No. APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN ANDIES COUNTR ZIP: COMPUTER MEDIUM COMPUTO APPLICA CURRENT APPLICA FILING CLASSI ATTORNEY NAME: REGIST REFERE TELECOMM TELEPH TELEPH TELEPH TYPE: INFORMATIO SEQUENCE LENGTUM MOLECULE US-07-7444-767	22 20 20 20 20 20 20 20 20 20 20 20 20 2	28
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cation US/077447  O  ION: John E. ggio, John E. mtyh, Patrick W. TION: Labelled TION: for Use i ENCES: Schwegman, Lundb O IDS Center apolis  BLE FORM: Floppy disk Floppy disk Floppy disk Floppy Token ETTER COMPATIBLE STEM: PC-DOS/MS AATION DATA: NUMBER: US/07/7 13-AUG-1991 ON: 435 ON: 435 ON: 435 ON: 435 ON: 435 ON: 13-AUG-1991 ON: 435 ON: 435 ON: 435 ON: 435 ON: 435 ON: 435 ON: 13-AUG-1991 ON: 435 ON:	444444444 0000000000000000000000000000	39
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RESULT 2 US-08-306-872-2

Sequence 2 Patent No.

Application US/08306872
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US-08-346-849-5
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                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08346849 Patent No. 5670483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Perlmutter, David H.
TITLE OF INVENTION: Method of Blocking the SEC Receptor
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
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NAME: Meyer_Scott J.

REGISTRATION NUMBER: 25,275

REFERENCE/DOCKET NUMBER: WU-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314,694-3117
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                            APPLICANT: Holmes, Todd
TITLE OF INVENTION: STAI
TITLE OF INVENTION: SELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                          NUMBER OF SEQUENCES: 6. CORRESPONDENCE ADDRESS:
                                                                                      STREET: INC.
CTTY: Lexington
"Assachus
                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                    STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                           ADDRESSEE:
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800 N. Lindbergh Blvd.
                                                                                                                        Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Lockshin, Curtis
                                                                                                                                                                                                                                                                Rich, Alexander
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100.0%; Pred. No. 0.
vative 0; Mismatches
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Best Local Similarity
Matches 11; Conserv
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Sequence 3, Approximately No. 5721106
                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Maggio,
APPLICANT: Mantyh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
                                                               TELEFAX: 612-305-1228 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         ZIP: 53430 ....
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/304,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/973,32
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NIMBER: 07/973,326
                               SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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LENGTH: 11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
TYPE: amino acid
STRANDEDNESS: no
                                                                                              TELEPHONE:
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P.O. Box 581415
                                                                              612-305-1228
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ER: MI
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Pred. No. 0.00035;
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Query Match

Length 11;

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-8
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Best Local Similarity
Matches 11; Conserv
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FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08302808 Patent No. 5750349 GENERAL INFORMATION:
                                                                                                                                                                                       TELEX: 200291 STRE INFORMATION FOR SEQ ID NO:
                                                                 TOPOLOGY
MOLECULE TYPE: pe
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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APPLICANT: DDAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/O FILING DATE: 15-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 24-JAN
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1 GSNKGAIIGLM 11
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                                                                                                                single
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00035;
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                                                                                                                                                                                             RESULT
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Best Local S
Matches 11
                                                                                                                           Sequence 5, Application US/08609090 Patent No. 5840838 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08433734 Patent No. 5837473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 612-305-122
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
      APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOY, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Maggio, John B.
APPLICANT: Mantyh, Patrick W.
APPLICANT: Mantyh, Labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 55458-1415
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11; Conserv
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GY: linear
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for Use in Detecting Alzheimer's Disease
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Pred. No. 0.00035;
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STREET: 99 Canaı CITY: Alexandria

ADDRESSEE: LOWE PRICE LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300

COUNTRY:

Virginia

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LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
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NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
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APPLICATION UNMERR: US/08/609,090
FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: DOS
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                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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1 GSNKGAIIGLM 11
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o. 5955317
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Similarity 100.0%; 1
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SYSTEM: PC-DOS/MS-DOS
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24-JAN-1994
                                    PCT/JP94/00089
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Pred. No.
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; ORIGINAL SOURCE:
US-08-986-948-8
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TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 22-AUG-1994
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOD
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                STREET: Two Mili
                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 02173-4799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
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5. 5955343
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Lockshin, Curtis
                                                                                                                                                                                                                                                                                                                                                                                                          Rich, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang,
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              MBER: 07/973,326
28-DEC-1992
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Best Local Similarity
Watches 11; Conserve
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US-09-005-215-10
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                                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICANT: Blanchard, Barbara J.
APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,188
FILING DATE: 29-OCT-1997
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,847
FILING DATE: 10-JAN-1997
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ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
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MOLECULE TYPE:
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                              TOPOLOGY: 1. MOLECULE TYPE:
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                                                          LENGTH: 11 amino acids
TYPE: amino acid
STRADEDNESS: single
                                                                                                                                                                                                  NAME: Gates, Edward R. REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
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GY: linear
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Pred. No.
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Best Local Similarity
Matches 11; Conserv
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GENERAL INFORMATION:
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ingram, Vernon M.
APPLICANT: Blanchard, Barbara J.
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STREET
APPLICATION NUMBER:
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: UNITED STATES OF AMERICA
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us/09/005,215
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Pred. No.
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TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

ENGTH:

: 14 amino acids amino acid

REFERENCE/DOCKET NUMBER: M0656/7035
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500

31,616

APPLICATION NUMBER: 08/98
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,6

PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

10-JAN-1997

60/035,847

08/960,188

PRIOR APPLICATION DATA:

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Best Local Similarity
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APPLICANT: Maggio,
APPLICANT: Mantyh,
                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                              TELEPHONE: 612-305-1217
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: LA
TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
MOLECULE TYPE:
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                   TELEPHONE: 612-305-1228
                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                          CITY: Minneapolis
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TOPOLOGY: 11
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Pred. No.
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APPLICANT:

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                            Sequence 6, Application US/08304585 Patent No. 5721106 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               MOLECULE TYPE: FRAGMENT TYPE:
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REFERENCE/DOCKET NUMBER: PP
TELECOMMUNICATION INFORMATION:
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NAME: Kara, Catherine J.
                APPLICANT:
                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                  19 GSNKGAIIGLM
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 Maggio,
Mantyh,
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IVENTION: modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggre
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Pred. No. 0.0011;
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Pred. No. 0.00084;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

112 113 114 114 115	Score Ma	Query Match Length		DB	ID	Description	otion
112 113 114 114 115	11 10	0.0	49	σ .	097917	097917	bos taurus
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# ALIGNMENTS

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RESULT
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Best Local Similarity
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01-JAN-1998
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                                                                                                                                                                                                                                                                                         01-MAY-1999 (TIEMBLIEL. 10, Created)
01-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation updata
AMYLOID PRECURSOR PROTEIN (FRAGMENT).
                          035463
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Pred. No. 3.7e-05;
Mismatches 0;
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Matches 11
                                                  Kamino K., Orr H. T., Payami H., Wijsman E.M., A Anderson L., O'dahl S., Nemens E., White J.A.; "Linkage and mutational analysis of familial Alkindreds for the APP gene region."; Am. J. Hum. Genet. 51:998-1014(1992).
EMBL; M29270; AAA51768.1; -.
EMBL; M29269; AAA51768.1; -.
EMBL; M15532; AAA51768.1; -.
EMBL; M25136; AAA5364.1; -.
EMBL; S45136; AAA5364.1; -.
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SEQUENCE
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MEDLINE-87120329; PubMed-2949367;
MEDZINE-B., Gusella J.F., Watkins P.C., Bruns G.A., C
Tanzi R.E., Gusella J.F., Watkins P.C., Kurnit D.M.,
Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M.,
"Amyloid beta protein gene: CDNA, mRNA distribution,
linkage near the Alzheimer locus.";
Science 235:880-884(1987).
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MEDLINE-89392030; PubMed-2675837;
Johnstone E.M., Chaney M.O., Moor
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      SEQUENCE
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Mammalia; Eutheria;
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(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 16, Last annotation updat)
TEIN (BETA-AMYLOID PROTEIN) (FRAGMENT)
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MEDLINE-93235601; PubMed=8476439;
MEDLINE-93235601; PubMed=8476439;
Denman R.B., Rosenzcwaig R., Miller D.L.;
PA system for studying the effect(s) of familial mutations on the processing of the beta-amyloid F mutations on the processing of the beta-amyloid F mutations. Res. Commun. 192:96-103(1993).
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MEDLINE=9335601; PubMed=8476439;

Denman R.B., Rosenzowaig R., Miller D.L.;

Passive for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor. "Biochem. Biophys. Res. Commun. 192:96-103(1993).

EMBL; S60721; AAB26263.2; -.

EMBL; P05067; 1BA4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
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Matches

Best Local Similarity

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RESULT 7
Q13778
ID 013778
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SEQUENCE
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Q16020;
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Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutations on the processing Biochem. Biophys. Res. Commu EMBL; S61383; AAB26265.2; -.
                                                                                                                                                                                       brain amyloid of Alzheimer's disease Science 235:877-880(1987).
                                                                                                                                                                                                                            Goldgaber D., Lerman M.I., McBride O.W., Saffion Characterization and chromosomal localization
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-87120328; PubMed-3810169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penman R.B., Rosenzcwaig R., Miller D.L.;
"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."; Biochem. Biophys. Res. Commun. 192:96-103(1993).
EMBL; S61383; AAB26265.2; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA APP
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Catarrhini;
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Pred.
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6.7e-05;
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RESULT
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          Coulson E.J., Paliga K., Beyreuther K., Ma
"What the evolution of the amyloid proteir
tells us about its function.";
Neurochem. Int. 0:0-0(2000).
EMBL; AF030341; AAF12698.1; -.
HSSP; P05067; 1BA4.
InterPro; IPRO1868; A4_APP.
Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; ANYLOIDA4.
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01-MAY-2000
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substrate for Caspase 3 in dying motoneurons.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF042098; AAC25052.1;
                                                                                                                                                                                                                                                                                                                                                                        APP
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Archosauria; Aves; Neognathae; Galliformes;
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01-JUN-2001
                                                                                                                                                                                                    TISSUE=BRAIN;
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nilarity 100.
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TEIN PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianidae
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Pred.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT)
MUS musculus (Mouse)
                                                                                                                          Thesis (2001), Department of Biological Sciences University of Nijmegen, Nijmegen, Netherlands. EMBL; AJ298150; CAC37193.1; -.
                                                                                                                                                                                Van den Hurk W.H.;
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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Strausberg R.;
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                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
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CAF1DF655C1AB653 CRC64;
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ia; Pipoidea; Pipidae;
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Ol-NOV-1996 (TIEMBLIEL 01, Las
Ol-JUN-2001 (TIEMBLIEL 17, Las
Ol-JUN-2001 (TIEMBLIEL 17) A4
ALZHEIMER'S DISEASE AMYLOID A4
Cavia porcellus (Guinea pig).
Eukaryotta Metazoa; Chordata; Chammalia; Eutheria; Rodentia; H
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InterPro; IPRO01868; A4_APP.
Pfam; PF02177; A4 EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
SWART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
SEQUENCE 695 AA; 78414 MW; 9
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STRAIN-SAMP8; TISSUE-HIPPOCAMPUS;
Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
Flood J.F., Kumar V.B., Sasser T., Word Addabases.
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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               Beck M., Mueller D., Bigl V.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: EUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDI
                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10141;
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Submitted (DEC-1996) to the
EMBL; U84012; AAB41502.1; -.
EMBL; U82624; AAB40919.1; -.
HRSP; P05067; 1QCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wragg M.A., Busfield Loring J.F., Goate A
                                                                                               TISSUE-BRAIN;
                                                                                                                   SEQUENCE FROM N.A.
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Pred. No.
                                                                                                                                                                                  Craniata; Vertebrata; Eut
Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I Sciurognathi; Muridae;
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                 GTP-BINDING
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Matches 11; Conserv
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-!- SIMILARITY: TO OTHER SPECIES AF
EMBL; X97631; CAA66230.1; -.
HSSP; P05067; IBA4.
InterPro; IPR001868; A4_APP.
Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; AM*LOIDA4.
SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
SEQUENCE 695 AA; 78701 MW; 519/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sarasa M., Rodolosse A., Sorribas V.;
Sarasa M., Rodolosse A., Sorribas V.;
"Cloning of full-length chicken beta-amyloid precursor protein isoforms.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF289218; AAG00593.1;
InterPro; IRP001868; A4_APP.
Pfam; PRO2177; A4_EXTRA; 1.
PR.NTS; PR00203; AMYLOIDA4.
SMART; SM00006; A4_EXTRA; 1.
SMOSITE; PS00319; A4_EXTRA; 1.
SROSITE; PS00319; A4_EXTRA; 1.
SROUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;
                                                                                                                                           Q98SF9 PRELIMINARY; PRT; 695 AA. Q98SF9; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BETA-AMYLOID PRECURSOR PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DGJ8;
                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chor
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                 APP.
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11; Conservative
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Neognathae; Galliformes; Phasianidae; Phasiani
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Search completed: April 24,
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Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
EMBL; AJ298151; CAC37194.1;
Signal.

1 18 POTENTIAL.
                                                                                                                                                SEQUENCE
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SEQUENCE FROM N.A.
                                                   621 GSNKGAIIGLM
                                                                                            Local Similarity
wes 11; Conserv
                                                              1 GSNKGAIIGLM
                                                                                                                                                 695 AA;
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; amyloid

R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra A;Reference number: PNO512; MUID:93290653
A;Accession: PN0512

beta-amyloid protein - guinea pig (fragment)
C;Speciles: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999
C;Accession: pN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya

RESULT PN0512

#### ALIGNMENTS

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A;Molecule type: mrNA
A;Residues: 1-57 </OH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal
C;Keywords: alternative splicing; Alzheimer's disease; amyloid;
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EG0045

RJohnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
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Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment) C. Species: Sus scrofa domestica (domestic pig) C. Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999 C. Accession: F60045 F. H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991 A. Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A. Reference number: A60045; MUID:92017079
A; Cross-references: EMBL:X56124
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
                                                                                                                            Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A; Reference number: A60045; MUID:92017079
A; Accession: D60045
A; Molecule type: mRNA
A; Residues: 1-57 < JOH>
                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment) c; Speciles: Bos primigenius taurus (cattle) c; Speciles: Bos primigenius taurus (lattle) c; Speciles: Bos primigenius taurus (lattle) c; Speciles: Bos primigenius taurus (lattle) c; Speciles: Bos primigenius (lattle) c; Speciles: Speciles: Bos primigenius (lattle) c; Speciles: Bos primigenius (latt
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Aizheimer's disease; amyloid; brain
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A; Title: Conservation of the sequence of the Alzheimer's disease amyloid A; Reference number: A60045; MUID:92017079
A; Accession: G60045
A; Molecule type: mRNA
A; Residues: 1-57 < JOH>
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 191
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A;Reference number: A60045; MUID:92017079
A;Accession: A60045
A; Molecule type: mRNA A; Residues: 1-57 < JOHN. A; Residues: 1-57 < J
                                                                                                                                                                                                                               A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide A;Reference number: A60045; MUID:92017079 A;Accession: B60045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragmen C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
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C;Superfamily: Alabairan'
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C; Date: 01
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A; Residues: 1-57 < JOH
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;Species: Canis lupus familiaris (dog)
;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
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Pred. No. 0.0028;
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                                   0.0028;
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                                          2;
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                                         Length 57
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proteinas

C;Accession: PQ0438; C60045 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E. Biochem. Biophys. Res. Commun. 188, 905-911, 1992 A;Title: Sequence and methylation in the beta/A4 region of t A:Reference number: PQ0438; MUID:93075180 Alzheimer's disease amyloid A4 protein precursor c; Species: oryctolagus cuniculus (domestic rabbit) C; Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 C; Accession: P00438; C60045 PQ0438 rabbit (fragment) #text\_change the rabbit amyloid 19-Oct-1995 precurs

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R; Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A; Title: Homology of the amyloid beta protein
A; Reference number: A49795; MUID:91273117
A; Accession: A49795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:M83558; GB:M03030;
A; Cross-references: GB:M83558; GB:M03030;
R; Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
R; Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
R; Johnstone, E.M.; Chaney, M.O.; 10, 299-305, 1991
A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
A: Poference number: A60045; MUID:92017079
R; de Strooper, B.; van Leuven, F.; van den Berghe, Blochim. Blophys. Acta 1129, 141-143, 1991 A;Title: The amyloid beta protein precursor or prot A;Reference number: S19727; MUID: 92096458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome
                                                                                                                                                                           A; Reference number: A27485; A; Accession: A27485
                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 149, 665-671, 198. A:Title: Complementary DNA for the mouse homolog
                                                                                                                                                                                                                                                              C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H
                                                                                                                                                                                                                                                                                                          N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989
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A; Residues: 1-695 < POD>
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A; Residues: 12-68 < JOH>
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A; Residues: 1-82 <DAV>
                                                                                    A; Experimental source: brain
                                                                                                       A; Residues: 1-695 < YAM>
A; Cross-references: GB: M18373; NID:g191568;
                                                                                                                                                         A; Molecule type: mRNA
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                                                                                                                                                                                                                                         H.; Miyata, T.; Goto,
9, 665-671, 1987
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A, Restruct. A. Experimental source: brain A, Experimental source: brain C; Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques C; Comperfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein C; Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein r.625-648/Domain: transmembrane #status predicted <TMM>
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A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695
A;Cross references: EMBL:X59379
R;Izumi, R; Yamada, T; Yoshikai, S; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the A;Reference number: I49485; MUID:9220998
A;Accession: I49485
                                                                                                                                                             A;Reference number: A39820;
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Schubert, D.; Schroeder, R.; LaCorbiere, Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is A;Reference number: A41245; MUID:88264430
A;Accession: A41245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seebur EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in A;Reference number: S00550; MUID:88312583
A;Accession: S00550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
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C; Superfamily: Alzhe
C; Keywords: alternat:
                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 266, 8464-8469, 19 A; Title: Purification and tissue
                                                                                                                                                                                                                                                                                                                                                       A;Note: rat peptides were isolated but not sequenced R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; M
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: The beta-A4 amyloid precursor protein A; Reference number: S46251; MUID:94320627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: evidence for heparan sulfate attachment R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, FEBS Lett. 349, 109-116, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
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A; Residues: 1-695 <SHI>
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C;Genetics:
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A; Residues: 1-19 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation; copper binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GSNKGAIIGLM 11
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                                                                                                                                                                                                                                                                                                                              266, 8464-8469, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease amyloid beta protein; ternative splicing; amyloid; transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                           issue level of MUID:91217087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                       the beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     possibly a
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                                                                                                                                                                                                                                                                                                                                                       Miller,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to copper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beyreuther, K.; Seeburg, P.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animal
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                                                                                                                                                                                                                                                                                                    peptide
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submitted to the EMBL Data Library, November 1988
A; Reference number: S05194
A; Reference number: S05194
A; Reference number: S05194
A; Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A; Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A; Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID A; Note: alternative splice form APP(695)
R; La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A; Title: Characterization of the 5'-end region and the first two A; Reference number: A32277; MUID:89165870
A; Residues: 1-75 <LAF>
A; Residues: 1-75 <LAF
A; Residues: 1-75 <LAF
A; Residues: 1-75 <LAF
A; Residues: 1-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease amyloid beta protein precursor [validated] - human N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inh N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu protein precursor splice form APP(770) c;Species: Homo sapiens (man) c;Species: Homo sapiens (man) c;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000 c;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A6681; A28583; A28902; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; A6681; A28583; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; A6681; A28583; A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-288, 'V', 365-770 <LEM1>
A; Cross-references: EMBL:X13466
A; Note: alternative splice form APP(695)
R; Lemaire, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Be Nucleic Acids Res. 17, 517-522, 1989
A; Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded A; Reference number: S02260; MUID:89128427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;/Superfamily: Alzheimer's disease amyloid beta C;/Keywords: alternative splicing; amyloid F;287-337/Domain: animal Kunitz-type proteinase
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C;Date: 10-Jun-1993 #seq
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
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A; Residues: 1-747 <OKA>
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A;Title: A Xenopus homologue of the human beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S52417;
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Matches
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;Species: Xenopus laevis (African clawed frog)
;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993
Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1;
Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.;
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Pred. No. 0.0
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R; Kang,
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A; Residues: 672-710 <PRE1>
A; Note: 693-Gln was found
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A; Residues: 687-718 < KAM2>
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A; Residues: 656-737 <LEV>
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A; Residues: 1-770 < YOS1>
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656-737 <JOH>
                                     Lemaire,
                                         H.G.;
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A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; F Blochem. Blophys. Res. Commun. 170, 301-307, 1990 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene A;Reference number: A35486; MUID:90321244
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A:Title: Genomic organization of the human A:Reference number: I39451; MUID:90236318
A:Accession: I39452
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 687-692, 'G', 694-718 <KAM1>
A; Residues: 687-692, 'G', 694-718 <KAM1>
A; Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1;
A; Experimental source: familial Alzheimer disease family SB
A; Note: sequence extracted from NCBI backbone (NCBIP:115374)
A; Accession: B44017
                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheime A;Reference number: A44017; MUID:93035397
A;Accession: A44017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
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A;Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:9178608; PIDN:AAB59501.1; PID:9178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
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A; Title: Alzheimer's disease amyloid peptide is
A; Reference number: A33260; MUID:89392030
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A; Residues: 689-716, 'F', 718-737 < MUR>
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A;Accession: I39453
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A; Title: Mutation of the Alzheimer's disease amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: revised physical map for reference R; Levy, E.; Carman, M.D.; Fernandez-Madrid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A59020; MUID: 91340168 A; Contents: annotation; erratum
                                                                                 A; Experimental source: familial Alzheimer disease family
                                                                                                              A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1;
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        sequence extracted from NCBI backbone (NCBIP:115376) this sequence has a silent mutation
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H.; Doh-ura, K.; Furuya, H.;
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  J.M.;
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Sakaki, Y
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W.E.; Pulst, S.M.; Anders
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R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distril
A;Reference number: A47585; MUID:87120329
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA5;
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA5;
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.I
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and
A;Reference number: S02638; MUID:88296437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S02638
A; Accession: S02638
A; Molecule type: mRNA
A; Residues: 672-678 cDYR>
A; Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.;
R; Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.;
Rature 331, 528-530, 1988
A; Title: Protease inhibitor domain encoded by an A; Reference number: S00707; MUID:88122640
A; Reference number: S00707
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 286-344, 'I', 365-366 <TAN2>
A; Cross-references: EMBL:X06982; NID:928817; PID:A; Cross-references: EMBL:X06982; NID:928817; PID:A; Cross-references: EMBL:X06982; NID:928817; PID:A; Note: alternative splice form APP(751)
R; Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.
Mature 331 525-527
                                                                                                                                                                                                                                                                                                                             A; Residues: 1-344,'I', 365-770 <PO2>
A; Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; A; Note: alternative splice form APP(751)
R; Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, Nature 331, 530-532, 1988
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A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288,'V',365-770 <KAN>
                                                                          A;Title: Novel precursor of Alzheimer's disease amyloid prot A;Reference number: A38949; MUID:88122641
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross references: GB:X06981; NID:928816; PIDN:CAA30041.1;
A;Cross referen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a doma A;Reference number: S00925; MUID:88122639
A;Accession: S00925
A;Molecule type: mRNA A;Residues: 1-344, 'I', 365-770 <PO2>
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                         Brain Res. Mol. I
A;Title: Absence
A;Reference numbe
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Science 235, 877-880, 1987
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A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
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                                                      mutation in the
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MUID:87120329
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a cell line HL60
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                                                      cDNAs cloned
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                                                                                                         Bartus, R.T.;
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                 C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision
C; Accession: C69971
R; Kunst, F.; Ogasawara, N.; Moszer, I.;
C.; Bron, S.; Brouillet, S.; Bruschi, C
A.; Ehrlich, S.D.: Emmarco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: BH1842
C;Superfamily:
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A; Experimental source:
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A; Residues: 1-247 <STO>
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A; Residues: 507-770 <ZAI>
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A; Status: not compan
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Residues: 606-770 <VIT3>
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~h, S.D.;
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                    Moszer, I.; Albertini, A.M.; Alloni, G.; Az
Bruschi, C.V.; Caldwell, B.; Capuano, V.;
P.T.; Entian, K.D.; Errington, J.; Fabret,
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A;Note: the authors translated the codon GAA for residue 8 as Val, GTG for residue 609 as Asn, AAT for residue 6 A;Note: the cited Genbank accession number, J03594, is R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser,
                                                                                                                                                                                                                              R; Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, A;Title: Molecular cloning of amyloid cDNA A; Reference number: A31087; MUID:88124954
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 122-288, 'V', 365-770
                                                                                                                                                     A; Cross-references: GB:M18734;
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Residues: 284-288,'V',365-770
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Conservative
                     100.0%;
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                                                                                                              NID:g178572; PIDN:AAA51726.1; PID:g178573 the codon GAA for residue 599 as Gly, ACC as Asn, AAT for residue 610 as Gly, and GC
                                                                                                                                                                                                                                                                                                                                                                                    <VIT2>
   0;
                                                                                                                                                                                                                                                                  G.; Sajdel-Sulkowska, E.M.; Majocha,
929-933, 1988
                       Pred.
                                     Score
 Mismatches
                       NO.
                                       54;
                                                                                                                                                                                                                                                  derived
                     0.035;
                                       DB 1;
   0;
                                     Length 770;
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                                                                                                                residue
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkal. 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 C;Accession: B83880 GB:AP001513; ce: strain Csequence of the 50; MUID:20263314 GB:BA000004; NID:g10174345; PIDN:BAB05561.1; 125 short-chain alkaliphilic BH1842 [imported] -G.; alcohol Sasaki, R.; Masui, N.; Fuji, #text\_change 31-Dec-2000 bacterium dehydrogenase Bacillus Bacillus halodurans halodurans GSPDB Ή : ŝ

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Similarity 80.0
8; Conservative
                                                                                    75.9%;
80.0%;
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2; Mismatches
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Bacillus subtilis
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05-Dec-1997 #text\_change 15-Oct-1999

Azevedo,

Carter,

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Nature 390, 249-256, 1997

A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y., M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Schrocker, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Serot akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Reference number: A69580; MUID:98044033
A.; Reference number: A69580; MUID:98044033
A.; Accession: C69971
A.; Coss-references: GB: Z99117; GB: AL009126; NID:92634966; PIDN:CAB14632.1; PID:e1183920; A.; Cepenturental source: Strain 168
C.; Genetics:
A.; Genetics: Strain 168
C.; Genetics: Strain 168
Search completed: April 24, 2002, 09:19:01 Job time: 200 sec
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q29149;
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Brain Res. Mol. Brain Res. 10:299-305(1991).
-I- FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIL
     PROTEIN
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Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
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Brain Res. Mol. Brain Res. 10:299-35(1991).
Brain Res. MOL. Brain Res. 10:299-35(1991).
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                    TISSUE=Brain,
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
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Best Local Similarity
Matches 11; Conser
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the Euro
                                                                                                                                                                  MEDLINE=92017079; PubMed=1656157;
Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-i- FUNCTION: FUNCTIONAL NEUGRONAL RECEPTOR WHICH COUPLES TO INTRACELULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIL TO THE COUPLES T
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Q28757;
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30-MAY-2000 (Rel. 35
ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
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-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING G(O) (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                             TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN (BETA-APP)
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PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Tran
NOW TEP
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE APP FAMILY.
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ween the swiss institute. The European Bioinformatics Institute. The European Bioinformatics as long
                                       SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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ilarity 100.
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SE AMYLOID A4 PROTEIN HOMOLOG
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Q28053;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 39, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."; Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTIONAL NEUROWAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Tran
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                                                                           HSSP; P05067; 1AML.
InterPro; IPR001868; A4_APP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                X56124; CAA39589.1;
X56126; CAA39591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X56130; CAA39595.1;
                                                                                                                                                                                                                  email to license@isb-sib.ch).
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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PROSITE;

PS00319; A4\_EXTRA; PARTIAL. PS00320; A4\_INTRA; PARTIAL. tein; Amyloid; Neurone; Tran

Transmembrane

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TISSUE=Liver, and Kidney;

MEDLINE=96108492; PubMed=8532114;

A Levy E., Amorim A., Frangione B., Walker L.C.;

T "Beta-amyloid precursor protein gene in squirrel monly cerebral amyloid anglopathy.";

RL Neurobiol. Aging 16:805-808(1995).

RL Neurobiol. Aging 16:805-808(1995).

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUCC
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Best Local
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SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
SMART; SM00131; KU; 1.
PROSITE; PS00321; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1;
                                                                                                               PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
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                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95241:
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS:
                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                 InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                 EMBL; S81024; AAD14347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saimiri sciureus (Common squirrel monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMYLOID PROTEIN (BETA-APP) (A-BETA)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE AFF CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restroy by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
WITH X11-ALPHA, BETA, AND -GAMMA, THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
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                                                                                                                                                                                    PF00117; A4_EXTRA; 1.
PF00014; Kunitz_BPTI; 1.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Platyrrhini;
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Pred. No.
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ni; Cebidae;
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                                                                                                                                                                                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A4_HUMAN STANDARD; PRT; 770; P05067; P09000; Q16011; Created) 13-AUG-1987 (Rel. 05, Created) 01-NOV-1991 (Rel. 20, Last sequence updatage of the control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
DOMAIN
                                                                                                                                                                         Lemaire H.G., Salbaum J.M., Multhaup G., Kang Unterbeck A., Beyreuther K., Mueller-Hill B.; "The PreA4(695) precursor protein of Alzheimer is encoded by 16 exons.";
                                                                                                                                                                                                                                                                                                                                                                                                         proteinase inhibitors.";
Nature 331:525-527(1988).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell-surface receptor ";
Nature 325:733-736(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B. "The precursor of Alzheimer's disease amyloid A4 protein recell-surface receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                              SEQUENCE FROM N.A. MEDLINE=97263807;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89128427;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A new A4 amyloid mRNA contains a proteinage inhibitors ":
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                              PubMed=9108164;
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                                                                                                                                      17:517-522(1989).
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CLATHRIN-BINDING (BY SIMILARITY).
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A4 PROTEIN.
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B W., Lieberburg
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N PRECURSOR (PROTEASE NEXIN-II)
D PROTEIN (BETA-APP) (A-BETA)].
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                                                                                                                                                                                                                                                                                         J.,
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                                                                                                                                                                                                                                                                                         Bayney R.M.,
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Fuller
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Hattori M.,

Tsukahara F.,

Furuhata

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Tanahashi H., Hirose

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A novel method for
sequencing of a 300
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"A novel m
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Gusella J.F., Neve R.L.;
                         "The
                                                                    Oltersdorf T., Fri
Johnson-Wood K.L.,
                                                                                         MEDLINE=89384866; PubMed=2506449; Oltersdorf T., Fritz L.C., Schenk
                                                                                                                                                                                MEDLINE-87250462; PubMed-3597385; van Nostrand W.E., Cunningham D.D.; van Nostrand of protease nexin II from J. Biol. Chem. 262:8508-8514(1987).
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Yoshikai S.-I., Sa
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Pardridge W.M., Vinters H.V., Yang J., Eisenberg
Tourtellotte W.W., Huebner V., Shively J.E.;
"Amyloid angiopathy of Alzheimer's disease: amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease brain:
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                                                 Sinha
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                       secreted
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precursor of Alzheimer's disease ar
se inhibitory activity.";
331:530-532(1988).
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Nature 3
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MEDLINE=90211252; PubMed=1969731;
Kido H., Fukutomi A., Schilling J., Wang Y., Cordell
"Protease-specificity of Kunitz inhibitor domain of
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MEDLINE=91104913; PubMed=2125487;
Hynes T.R., Randal M., Kennedy L.A.,
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MEDLINE=88296437;
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Poulsen S.-A., Wat
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MEDLINE=94281210; PubMed=7516706;
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5582; PubMed=10201399;
Cappai R., Feil S.C., Her
Hesse L., Multhaup G., Bey
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                               130:142-152(2000)
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moto T., Matsuura
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 PubMed=2900137;
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MEDLINE-89345111; PubMed-2569710;
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Sakai Y.;
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Science 256:780-783(1992).
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                                                                                                                                                                                                                                                                                                                                                                   Yamada T., Sasaki H., Furuya H., Miyata T., Goto "Complementary DNA for the mouse homolog of the h
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88106489;
Yamada T., Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-OCT-1989 (Rel. 12, Created)
Ol-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG
(AMYLOIDOGENIC GLYCOPROTEIN) (AG).
                                                                                                              SEQUENCE OF 1-19 FROM
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                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92096458; PubMed=1756177;
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/C; TISSUE-Brain;
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H., Furuya H.,
                                                                             PubMed=1555768;
f., Yoshikai S.I.,
                                                                                                                                                                                                                                                                                                                                       Res.
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Rodentia;
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EMBL;
EMBL;
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-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PR
-i- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(39
APP(751) AND APP(770) (SHOWN HERE); ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 281-380 FROM N.A., AN TISSUE-Brain, and Kidney:
MEDLIKE-89119813; Pubm6d-2493250;
Yamada T., Sasaki H., Dohura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.; "Structure and expression of the alternatively-spliced for the mouse homolog of Alzheimer's disease amyloid be
                                                                                                                                                                                                                           between
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TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY.
WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KI
                                                                                                                                                                                               ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE APP FAMILY.
SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIAN WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO REPTIDE RESIDUES THAT ARE C-TERMINAL TO NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
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een the Swiss Institute of Bio
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ISOFORMS; APP(395), APP(SHOWN HERE); ARE PRODUCED
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KIDNEY AND
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MGD: MGI: 88059; App.
InterPro; IPR001868; A\_APP.
InterPro; IPR002223; Kunitz\_BPTI
InterPro; IPR002223; Kunitz\_BPTI;
Pfam; PF00217; A4\_EXTRA; 1.
Pfam; PF00014; Kunitz\_BPTI; 1.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE. PIR: A27485; A27485. PIR: S04855; S04855. PIR: S19727; S19727. MGD; MGI:88059; App. CARBOHYD CARBOHYD VARSPLIC VARSPLIC VARSPLIC SITE DISULFID DISULFID DISULFID TRANSMEM DOMAIN CHAIN PROSITE; PS00319; A4\_EXTRA; 1.
PROSITE; PS00320; A4\_INTRA; 1.
PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.
PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; EMBL; DOMAIN DOMAIN DOMAIN SIGNAL Alternative SMART; SM00006; SMART; SM00131; X59379; -; NOT\_ANNOTATED\_CDS M18073; AAA377.39.1; -X15210; CAA33280.1; -D10603; BAA01456.1; -D10603; BAA01456.1; -M24397; AAA39929.1; -700 724 673 287 759 291 300 316 542 542 571 289 290 346 splicing; A4\_EXTRA; KU; 1. 699 7723 7715 715 345 345 347 341 324 324 324 324 324 324 380 571 542 571 589 380 86752 Kunitz\_BPTI. Serine ₩; BY SIMILARITY.
BY SIMILARITY. N-LINKED (GLCNAC. . .) (POTENTIAL).

LINKED (GLCNAC. . .) (POTENTIAL).

E -> V (IN ISOFORM APP(695)).

MISSING (IN ISOFORM APP(695)).

MISSING (IN ISOFORM APP(751)).

26C50DE0890CAF7A CRC64; BPTI/KUNITZ INHIBITOR CLATHRIN-BINDING (BY protease inhibitor.
BY SIMILARITY. CYTOPLASMIC (F POTENTIAL EXTRACELLULAR ALZHEIMER'S HOMOLOG. SIMILARITY. DISEASE AMYLOID BETA-AMYLOID (POTENTIAL) Signal; SIMILARITY). A4

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RESULT
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                                   PIR; S03607; S03607.
InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
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P08592;
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PIR;
                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=10116;
[1]
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01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMO
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         PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00204; BETAAMYLOID.
PRINTS; PR00759; BASICPTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Alzheimer's disease amyloidogenic glycoprotein: in rat brain suggests a role in cell contact."; EMBO J. 7:1365-1370(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seeburg P.H.;
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SPLICING.

DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA, THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY.)

SIMILARITY: BELONGS TO THE APP FAMILY.

SIMILARITY: CONTAINS 1 BPTL/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                  by non-profit institutions as long
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ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(551) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
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$03607; $03607
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SM00006; A4_EXTRA;
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Best Local S
Matches 11
SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
STRAIN-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ol-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN D
DPPC OR B3542 OR Z4959 OR ECS4422.
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_ECOLI
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VARSPLIC
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SEQUENCE
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DISULFID
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DOMAIN
                                                                                                                                                  Nucleic [3]
                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / MM500;
MEDLINE=95231288; PubMed=7536291;
Abouhamad W.N., Manson M.D.;
"The dipeptide permease of Escherichia coli closely resembles other
bacterial transport systems and shows growth-phase-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli, and
Escherichia coli O157:H7.
Bacteria, Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00280; BPTI_KUNITZ_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
                                                                                                                                                              Sofia H.J., Burland V., Daniels D.L., Plunkett "Analysis of the Escherichia coli genome. V. DN region from 76.0 to 81.5 minutes."; Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P37315;
01-OCT-1994
                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N. STRAIN-K12 / MG1
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                                                                                                                                                                                                                                                                                                                                               expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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BY SIMILARITY.
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N-LINKED (GLCNAC...) (POTENT
E -> V (IN ISOFORM APP(695))
MISSING (IN ISOFORM APP(695)).
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Pred. No.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALZHEIMER'S DISEASE AMYLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C26C9D6BB2D929A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                       DNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
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                                                                                                                                                                                                                              III, Blattner
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Best Local
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                                         CBL_HUMAN STANDARD; PRT; 906 AA P22681; 01-AUG-1991 (Rel. 19, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat SIGNAL TRANSDUCTION PROTEIN CBL (PROTO-ONCO CBL OR CBL2.
                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Tanakami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DIA Res. 8:11-22(2001).
-I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grotbeck E.J., Davis N.W., Lim A., Dima Apodaca J., Anantharaman T.S., Lin J., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
Eukaryota; Metazoa;
Mammalia; Eutheria;
       CBL OK CDL...
Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport;
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                                                                                                                                                                                                                                                                   Local Similarity
nes 6; Conser
                                                                                                                                                                                                                                      3 NKGAIIGLM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR DIPERTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
SUBSTRATE ACROSS THE MEMBRANE PROTEIN. INNER MEMBRANE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L08399; AAA23704.1; -.

J00039; AAB18520.1; -.

AE000431; AAC58686.1; -.

AP002565; BAB37845.1; -.
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                                                                                                                                                                                                        NKGAVVGLV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00528;
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137
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300 AA;
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 Primates;
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66.7%;
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                                                                                                                                                                                                                                                                                              Score 38;
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
C4DD7BD82286EE62 CRC64;
 Catarrhini; Hominidae;
               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                          (PROTO-ONCOGENE C-CBL).
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                  No.
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J., Yen G., Schwartz
                                                                      update)
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3.9;
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                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                             Length 300
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RESULT 13
RS1B_SYNY3
ID RS1B_S
AC P74142
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Best Local
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InterPro; IPR001841; Znf_rin
Pfam; PF02262; Cbl_N; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                         MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91232862; PubMed-2030914; Blake T.J., Shapiro M., Morse H.C. III, Langdon W.Y.; Blake T.J., Shapiro M., Morse H.C. III, Langdon W.Y.; "The sequences of the human and mouse c-cbl proto-oncogenes show v-cbl was generated by a large truncation encompassing a proline domain and a leucine zipper-like motif."; oncogene 6:653-657(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                             SMART; SM00184; RING; SMART; SM00165; UBA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: ASSOCIATES WITH NCK VIA ITS SH3 DOMA
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PTM: PHOSPHORYLATED ON TYROSINE.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 UBA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the amino-terminal domain of Cbl complexed binding site on ZAP-70 kinase.";
Nature 398.84-00/1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X57110; CAA40393.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 398:84-90(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) MEDLINE=99176421; PubMed=10078535;
                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                        3D-structure
                                                                                                                                                                                                                                                                                                                    Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                            19
                                                                                                   1 GSNKGAIIGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC CELLS. ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR MANY SIGNALLING PATHWAYS THAT START FROM RECEPTORS AT THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SURFACE.
                                                                           GSGSGGLIGLM
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                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                  PS00518;
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                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                      Nuclear
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i; 1.
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                                                                                                                                                                                          PHOSPHORYLATION.
PHOSPHORYLATION.
; 7D686B050204AD8F CRC64;
                                                                                                                                         Pred.
                                                                                                                                                     Score 37;
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ASP/GLU-RICH
                                                                                                                                                                                                                                                                    ASP/GLU-RICH
                                                                                                                                                                                                                                                                                 RING-TYPE
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                                                                                                                             Mismatches
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                                                                                                                                         No.
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RS1B\_SYNY3 P74142;

STANDARD;

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CBL_MLYCN
ID CBL_M
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OS CAS-N
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P23092;
01-NOV-1991
01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003029; S1. Pfam; PF00575; S1; 3. SMART; SM00316; S1; 3.
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RPS1B
                                                                                                                                                           Cas-NS-1 murine leukemia virus Viruses; Retroid viruses; Retro NCBI_TaxID=11793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocystis sp. (straing Bacteria; Cyanobacteria; NCBI_TaxID=1148;
                                                                                                                                                                                                                         V-CBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 3:109-136(1996).
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01-NOV-1997 (Rel.
20-AUG-2001 (Rel.
                                   Morse H.C. III;
"v-cbl, an oncogene from
                                                            Langdon W.Y., Hartley
Morse H.C. III;
                                                                                                                                                                                                                                              TRANSFORMING
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                                                                                               SEQUENCE FROM N.A. MEDLINE=89145204; PubMed=2784003;
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1B OR SLR1984.
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steria; Chroococcales;
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  86:1168-1172(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358C35F778BE03F5 CRC64;
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RESULT 15
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97080510; PubMed-8921855;
MEDLINE-97080510; PubMed-8921855;
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20-AUG-2001 (Rel. 40, Last ann
GALACTOSIDE TRANSPORT ATP-BIND
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InterPro; IPR003153; Cbl_N.
Pfam; PF02262; Cbl_N; 1.
Transforming protein; Oncogene.
SEQUENCE 390 AA; 43692 MW; EB72
                                                                                                                                                       "Complete genome sequence of Treponema pallidum, spirochete."; Science 281:375-388(1998).
                                                                                                                                                                                                             Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
                                                                                                                                                                                                                                                                                                                                                          Porcella S.F., Popova T
Norgard M.V.;
"A mgl-like operon in T
Gene 177:115-121(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      Fraser C.M., Norris S.J., Weinstock G.M., White O., Sundson R., Gwinn M., Hickey E.K., Clayton R., Ketchum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum.
Bacteria; Spirochaetales;
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                                                                                  ence 281:375-388(1998).

FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT FOR GALACTOSIDES. PROBABLY RESPONSIBLE FOR ENERG THE TRANSPORT SYSTEM (BY SIMILARITY).

SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTEN SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT
s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: CBL INDUCES EARLY B-LINEAGE LYMPHOMAS. MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-CBL
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                                                                     TRANSPORTERS). MGLA/RBSA SUBFAMILY.
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                                                                                    BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
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63.6%;
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ATP-BINDING PROTEIN MGL
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18;
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mith H.O.
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                                                                               SPTREMBL_17:*
1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score 54	Query Match 100.0	Query Query Match Length	DB 6	ID 097917 035463
	5 <b>4</b>	100.0	82 82	4 4	Q16014 Q16019
6	54	100.0	. 82	4	Q16020
7	54	100.0	97	4	Q13778
æ	54	100.0	534	13	093296
9	54	100.0.	569	13	Q9PVL1
10	54	100.0	607	11	Q99K32
11	54	100.0	693	13	Q98SG0
12	54	100.0	695	11	P97487
13	54	100.0	695	11	Q60496
14	54	100.0	695	13	д9рсл8
15	54	100.0	695	13	Q98SF9
16	54	100.0	699	13	057394
17	54	100.0	737	13	093279
18	54	100.0	747	13	691963
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# ALIGNMENTS

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01-MAY-1997
01-MAR-2001
                                                    Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Puls Anderson L., O'dahl S., Nemens E., White J.A.;

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Am. J. Hum. Genet. 51:998-1014(1992).

EMBL; M29270; AAA51768.1;

EMBL; M29269; AAA51768.1;

EMBL; M1533; AAA51564.1;

EMBL; S45136; AAA631564.1;

EMBL; S45136; AAA63646.1;
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SEQUENCE OF 19-48 FROM N.A.
MEDLINE-87120329; PubMed=2949367;
Tanzi R.E., Gusella J.F., Warkins P.C., Bruns G.A., G
Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M.,
"Amyloid beta protein gene: cDNA, mRNA distribution,
linkage near the Alzheimer locus.";
Science 235:880-884(1987).
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Mammalia; Eutheria;
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Johnstone E.M., Chaney
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MEDLINE=93236601; PubMed=8476439;
MEDLINE=93236601; PubMed=8476439;
Denman R.B., Rosenzcwaig R., Miller D.L.;
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MEDLINE=93256601; PubMed=8476439;

Denman R.B., Rosenzowaig R., Miller D.L.;

Paraman R.B., Rosenzowaig R., Miller D.L.;

"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor."

Biochem. Biophys. Res. Commun. 192:96-103(1993).

EMBL; S60721; AAB26263.2; -.

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93236601; PubMed=8476439; Denman R.B., Rosenzcwaig R., Miller D.L.; "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor." Biochem. Biophys. Res. Commun. 192:96-103(1993). EMBL; S61383; ABAS6265.2; -. EMBL; S61383; ABAS6265.2; -. HSSP: P05067; 1BA4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NAR-2001 (TrEMBLrel. 16, Last annotation
BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                   MEDLINE-87120328; PubMed-3810169; Goldgaber D., Lerman M.I., McBride O.W.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Best Local S
Matches 11
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      093296;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLREL. 17,
ANYLOID PRECURSOR PROTEIN ()
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordat;
                                                                                                                                                                                                                                                                                                                                                                                            "Increased production of amy
substrate for Caspase 3 in d
submitted (JAN-1998) to the
EMBL; AF042098; AAC25052.1;
HSSP; P05067; 1BA4
                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Metazoa; Chordata;
                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AMYLOID PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001868; A4_APP.
PRINTS; PR00203; AMYLOIDA4.
PROSITE; PS00319; A4_EXTRA;
PROSITE; PS00320; A4_INIRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Barnes N.Y., Ling L., Milligan C.E.;
                                                                                       TISSUE-BRAIN;
                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                 Q9PVL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    093296
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                  Archosauria;
                                                                                                                                                                                                        Q9PVL1;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                            460
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| GSNKGAIIGLM
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 SM00006;
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Similarity 100.
11; Conservative
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                                                                                                                                  Aves;
                                                                                                                                                                                                                                                                                                                                         AA;
 A4_EXTRA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neognathae;
                                                                                                                                  Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                         60597 MW;
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in dying
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Last annotation updat
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                                                                                                                                                                                                                                                                                             Score 54; DB
Pred. No. 0.0
); Mismatches
                                                                                                                                Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Veri; Galliformes;
                                                                                                                                                                                                                 PRT;
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                                                                    r K., Masters
protein precu
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nes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                DB 13;
                                                                    precursor
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                                                                                                                                  Phasianinae;
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                                                                     family
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Best Local
Matches 1
Query Match
Best Local Similarity
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PROSITE;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99K32;
                                                                                                                 Van den Hurk W.H.;
Van den Hurk W.H.;
Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
EMBL; AJ298150; CAC37193.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                           SEQUENCE
                                                                                                           Signal.
                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrach
                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT)
Mus musculus (Mouse)
                                                                                              SIGNAL
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    APP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98SG0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                         298SG0;
                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                          Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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PS00320;
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A4_INTRA;
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Rodentia;
                                                                         18 I
78568 MW;
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Pred. No. 0.0
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CAF1DF655C1AB653
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Pred.
Score
Pred.
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Sciurognathi;
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0.084;
 DB 1
0.11;
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; Murinae; Mus
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Loring J.F., Goate A.M.;
Submitted (DEC-1996) to the EMBL
EMBL; U84012; AAB41502.1; -.
EMBL; U84012; AAB41502.1; -.
HSSP; P05067; 1QCM.
HSSP; P05067; 1QCM.
HSSP; P052177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOJDA4.
SMART; SM00006; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                       01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                       Q60496;
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01-MAY-1997
01-JUN-2001
                                                                                                                                                                      Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SAMPB; TISSUE-HIPPOCAMPUS;
Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                Beck M., Mueller D., Submitted (JUN-1996)
                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                             01-NOV-1996 (TIEMBLEEL 01, Created)
01-NOV-1996 (TIEMBLEEL 17), Last sequence update)
01-JUN-2001 (TIEMBLEEL 17, Last annotation updat
ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                           TISSUE-BRAIN;
                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129SV;
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                      k M., Mueller D., Bigl V.;
mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BIND
  G(0)
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ll; Conservative
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Rodentia;
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Pred. No.
                                                                                                                                                                                                Craniata; Vertebrata;
Hystricognathi; Cavii
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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; Murinae; Mus
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RESULT Q98SF9 ID PT 0: DT 0: D
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RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AR289218; AAG00593.1; -
DR InterPro; IPR001868; A4_APP.
DR FIAM; 1.
DR PFIAMT; PR02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR ROSITE; PS00319; A4_EXTRA; 1.
DR ROSITE; PS00319; A4_EXTRA; 1.
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Matches 11
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Best Local Similarity
Matches 11; Conserva
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C -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
R EMBL; X97631; CAA66230.1; -.
R HSSP; P05067; 1BA4.
R HIGEPPO; IPRO01868; A4_APP.
R FEAM; PE02177; A4_EXTRA; 1.
R PRINTS; PR00203; AMYLOIDA4.
R SMART; SM00006; A4_EXTRA; 1.
R PROSITE; PS00319; A4_EXTRA; 1.
R PROSITE; PS00319; A4_INTEA; 1.
SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
                                                                                                                                                        Q98SF9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
BETA-AMYLOID PRECURSOR PROTEIN B.
                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                          Q98SF9
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                             Xenopus.
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Pred. No. 0.11;
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                                                       Query Match
Best Local :
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                                                                                                              Van den Hurk W.H.;
Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
EMBL; AJ298151; CAC37194.1; -.
Signal.

1 18 POTENTIAL.
                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                    SEQUENCE
1 GSNKGAIIGLM 11
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621 GSNKGAIIGLM 631
                                                       Local Similarity
                                           11;
                                                                                                     695 AA;
                                           100.0%; ilarity 100.0%; Conservative 0
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                                                       Score 54; DB 13; Length 695; Pred. No. 0.11;
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Search completed: April 24, 2002, 09:20:11 Job time: 240 sec

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Result
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                           Length
    30
318
318
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166
                                                                                                                                                                                             DB
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      118
121
121
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123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chosen parameters:
                 AAY09349
AAY52134
AAW44200
AAW33754
AAY52130
AAW44199
AAW33753
AABB1925
AAW44214
AAW33768
                                                                                                                                                                                           Π
                                                                                                                                                                                                                                       SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (without alignments)
33.406 Million cell updates/sec
Human RAGE polypep
Extracorporeal cir
Human soluble RAGE
Human RAGE polypep
Human soluble RAGE
                                                                                                                                                                                          Description
                                                                              Human
                                                                                                Human
                                                                                                              Human
                                                                                                                             Human
                                                                                                                                                           Human RAGE V-domai
                                                                                                                                              Human
                                             n mature recep
n RAGE polypep
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n soluble rece
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                                                                                                                                            Receptor to
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	6 20																																15 50
.0 481		_	. ~					4	.0 399														.0 30								.7 30	.3 30	.0 15
21	21	19	16	21	21	21	22	21	16	21	22	19	21	21	21	21	21	21	22	20								18	18	18	20	20	18
AAG50448	AAG20757	AAW40814	AAR71033	AAG50449	AAG20758	AAG52002	AAB85144	AAG52003	AAR71032	AAG52004	AAB73217	AAW60564	AAG54141	AAG22864	AAG54142	AAG22865	AAB41577	AAG57767	AAM36735	AAW92647	AAW27362	ÀАВ36499	AAW23337	AAY09352	AAY52135	AAY09353	AAW33755	AAW33763	AAW44201	AAW44209	AAY09351	35	AAW33762
Arabidopsis thalia	Arabidopsis thalia	Human 5-HT2B recep	G protein protein				Human NKCR polypep	Arabidopsis thalia	G protein protein	Arabidopsis thalia	Murine phosphatase	н	Arabidopsis thalia			Arabidopsis thalia	Human ORFX ORF1341	Arabidopsis thalia	Peptide #10772 enc	-1 pepti	Residues 138-147 o	Acinetobacter sp.	N-terminal seqeunc	Œ.	Recep	RAGE	RAGE polype	RAGE polype	soluble	Human soluble RAGE	AGE V-	RAGE V-doma	Human RAGE polypep

# ALIGNMENTS

AAY09349

AAY09349 standard; peptide;

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09-JUL-1999 (first entry)

AAY09349

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RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
          WPI; 1999-277439/23.
                                                                                                   09-OCT-1998;
                                                                                                                                                                                          neuropathy;
                                                                                                                                                                                                                 neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
                                                                             09-OCT-1997;
                                                                                                                         22-APR-1999.
                                                                                                                                                WO9918987-A1
                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                     Human RAGE V-domain peptide SEQ ID NO:1.
                                                                                                                                                                                                        tumour;
                                                     (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                          cancer; male impotence; wound healing;
thy; retinopathy; nephropathy; neuronal
                                Ļ
                               Schmidt AM,
                                                                             97US-0948131.
                                                                                                    98WO-US21346.
                                 Stern D,
                                 Yan
                                SD;
                                                                                                                                                                                           periodontal disease; degeneration.
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RESULT
AAY52134
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibiting formation of an ABP fibril on a cell; (4) inhibiting extracellular assembly of an ABP into a fibril; (5) inhibiting aggregation of ABP on the surface of a cell; (6) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a microglial cell by an ABP; (8) treating a subject with a condition associated with an interaction of an ABP with a receptor for RAGE on a cell; (9) evaluating the ability of an agent to inhibit binding of an ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting periodontal disease in a subject; (12) inhibiting an RAGE's interaction with a receptor for RAGE when the receptor is on the surface of a cell; and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble receptor for advanced glycation endproducts; invasion; metastasis; amphoterin; neuron; inhibit; the solution of the so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an aucum
wound healing, perro
mound degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an autoimmune disease, inflammation, a tumour, cancer, male impotence, wound healing, periodontal disease, neuropathy, retinopathy, nephropat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE, e.g. diabetes, Alzhelmer's disease, seniity renal failure, hyperlipidaemic atherosclerosis, contractivity of the conditions 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Also described are methods for: (1) inhibiting an amyloid-beta peptide (ABP) interaction with a receptor for RAGE when the receptor is on the surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides based on an advanced glycation end product receptor are useful for treating Alzheimer's disease and Down's syndrome
WPI; 2000-013260/01
                                                                                Schmidt AM,
                                                                                                                                                                                                                                                         17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09954485-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY52134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY52134 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V-domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes novel
                                                                                                                                                                (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
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f a receptor for an advance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AA;
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                                                                                    Stern D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                         98US-0062365
                                                                                                                                                                                                                                                                                                                                              99WO-US08427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGE (RAGE) amino acid sequence fragment #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
4e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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prevents receptor bir permeability, useful

Claim 2; Page 42-43; 90pp; English

Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus

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This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective invasion and metastasis via administration of a therapeutically effective
                                                                            amount of the pharmaceutical composition containing a RAGE polyper The invention also relates to a method for evaluating the ability agent to inhibit tumour invasion in a local cellular environment. can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 29; Page 62;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts -
                                                      carrier.
30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88pp; English.
                                                                                                                                                               polypeptide
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RESULT
AAW44200
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                                                                                                                                                                                                                                                                                                                                        Query Match
                                       WPI; 1997-558580/51.
N-PSDB; AAV12395.
                                                                                                         11-APR-1997;
                                                                                                                                    WO9739125-A1
                                                                                                                                                                                                                 Human mature receptor to an
                                                                                                                                                                                                                               14-MAY-1998
                                                                                                                                                                                                                                             AAW44200;
                                                                                                                                                                                                                                                           AAW44200 standard; Protein;
                                                              Hollander DA,
                                                                            (SCHD ) SCHERING PATENTE AG
                                                                                           16-APR-1996;
                                                                                                                      23-OCT-1997
                                                                                                                                                          Misc-difference
                                                                                                                                                                                                   Human; soluble
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                            w
                                                                                                                                                                              sapiens
                                                                                                                                                                                            antibody;
                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                            receptor; advanced glycosylation end product; RAGE; vascular permeability; diabetes mellitus.
                                                              Morser
                                                                                          96US-0633148
                                                                                                         97WO-EP01834
                                                                                                                                                         Location/Qualifiers 66
                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                              Ŋ,
                                                                                                                                                   "encoded by CCT"
                                                              Nagashima
                                                                                                                                                                                                                 advanced glycosylation end product.
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                 Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                 4e-25;
                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                                                                                                                          Indels
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B 8

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Matches
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Best Local
                        This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (318 amino acid residues). The RAGE polypeptides and its active fragments or their mimetics, inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular disorders such as neuropathy, nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated amyloidosis, also activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. maiorives culopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a mature human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with
                                                                                                                                                                                                                                                                                                                                                                            New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-526458/48.
N-PSDB; AAV06518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW33754 standard;
                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morser MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Advanced glycosylation end-product receptor; RAGE; screening; AGE; vascular permeability; diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human RAGE polypeptide (318 amino acid residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW33754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolation and purification of human RAGE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aqnitarigeplvlkckgapkkppqrlewk 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
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                                                                                                                                                                                                                                                                                                                     Fig 1B; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagashima
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sis) or hae
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   beta-amyloid
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Pred. No. 2.8
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   Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Best Local :
                                                                         considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture at to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of the compounds of the compound of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble receptor for advanced glycation endproducts; RAGE; tumour; invasion; metastasis; amphoterin; neuron; inhibit; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                        can be
                                                                                                                                                                                                                                                                                                                                              Advanced Glycation Endproducts (RAGE). RAGE interacts with a range physiologically and pathophysiologically relevant ligands when
                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the human soluble Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts - {\color{black} }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-013260/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 10-11;
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                                                     to a patient in a pharmaceutically acceptable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local
                                                                                                                                                             The present sequence represents a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
                                                                                                                                                                                                                                                                                       Claim 2; Page 40-41; 90pp; English.
                                                                                                         Sequence
                                                                                                                                         vascular disorders, neuropathy, nephropathy, retinopathy, haemodia associated amyloidosis or atherosclerosis. The Ab can also be used
                                                                                                                                                                                                                                                                                                                         Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular
                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                               associated amyloidosis or atherosclerosis.
the isolation and purification of human RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1996;
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23
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                      AQNITARIGEPLVLKCKGAPKKPPQRLEWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble receptor to an advanced glycosylation end product
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                                               Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                               to treat diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 AA
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                                                                                                                                 RAGE
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                                                                                                                              polypeptide.
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AAW33753
                                                age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                           disorders such as neuropathy, nephropathy, retinopathy or atherosclerosis) or haemodialysis associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or
                                                                                                                                                                                                                                                             This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (340 amino acid residues). The RAGE polypeptides and its active fragments or their mimetics, inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Advanced glycosylation vascular permeability; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human RAGE polypeptide (340 amino acid residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-526458/48
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diabetes mellitus; treatmen
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Best Local :
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a material for extracorporeal circulation which is made from a water-insoluble carrier immobilized with a protein having the sequence shown here. The materials of the invention, including adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body
                                                                      Human; soluble receptor; advanced glycosylation end AGE; antibody; vascular permeability; immunologicall diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                          fluid, and are therefore useful in treating vascular lesions arteriosclerosis due to carbonyl stress products caused by alpromoted carbonyl stress from excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracorporeal circulation; carbonyl stress product; diabetes; vascular lesion; excretory dysfunction.
                                                                                                                                                                      AAW44214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dysfunction in vascular lesions
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                       W09739125-A1
                                              Homo sapiens
                                                                                                                       Human soluble
                                                                                                                                              14-MAY-1998
                                                                                                                                                                                              AAW44214 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracorporeal circulation material receptor protein
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                                                                                                                      RAGE
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                                                                                                                    immunologically active fragment SEQ ID NO:18.
                                                                                                                                                                                              peptide;
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immunologically active fragment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an immunologically active fragment of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (RGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Advanced glycosylation end-product receptor; RAGE; screening; AGE; vascular permeability; diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                       Morser MJ,
                                                                                                                                                                                                                                 (SCHD
                                                                                                                                                                                                                                                                                                                                 16-APR-1996;
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Pred. No.
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2e-10;
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active fragments or their minmetics can inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular disorders such as neuropathy, nephropathy, atherosclerosis or retinopathy) or haemodialysis-associated amyloidosis, also activation of microgilal cells by beta-amyloid peptides in Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etc.,
             Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                           11-APR-1997;
                                                                                                                                                                                                                                                                                                                                      diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                Human; soluble receptor; advanced glycosylation end product; AGE; antibody; vascular permeability; immunologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes
                                                                                                                                                                                                                                          23-OCT-1997
                                                                                                                                                                                                                                                                      W09739125-A1
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Human soluble RAGE immunologically active fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                           (SCHD
                                                                                                                                                                           16-APR-1996;
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                                                                                                            Morser MJ,
                                                                                                                                                                         96US-0633148
                                                                                                                                                                                                           97WO-EP01834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                            Nagashima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16;
Pred. No.
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2e-10;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Advanced
vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.
        This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active fragments or their mimetics can inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular disorders such as neuropathy, nephropathy, atherosclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an immunologically active for a soluble human receptor to an advanced glycosylation ensproduct (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with
                                                                                                                                                                               New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabete etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW33762 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RAGE polypeptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1998
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                                                                                                                                                     Claim 6;
                                                                                                                                                                                                                                               WPI; 1997-526458/48
                                                                                                                                                                                                                                                                                                                                        16-APR-1996;
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                                                                                                                                                                                                                                                                                                        (SCHD ) SCHERING
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                                                                                                                                                    Page 55; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycosylation permeability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 46; 90pp;
                                                                                                                                                                                                                                                                           Nagashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                        96US-0633147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end-product receptor; RAGE; s
diabetes mellitus; treatment;
                                                                                                                                                    English.
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hes 0;
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retinopathy) or haemodialysis-associated amyloidosis,

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Best Local
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Also described are methods for: (1) inhibiting an amyloid-beta peptide (ABP) interaction with a receptor for RAGE when the receptor is on the surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) inhibiting formation of an ABP fibril on a cell; (4) inhibiting extracellular assembly of an ABP into a fibril; (5) inhibiting aggregation of ABP on the surface of a cell; (6) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a
                                                                                                                                                                                                                        The present invention describes novel isolated peptides (I) having a amino acid sequence corresponding to an amino acid sequence of a V-domain of a receptor for an advanced glycation end product (RAGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; amyloidosis; autoimmune disease; tumour; cancer; male impotence; wound healing; period
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   senility; renal failure; hyperlipidaemic atherosclerosis; dementia neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides based on an advanced glycation
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                                                                                                                                                                                                                                                                                                                                                                                                                             treating Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V-domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt AM,
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                                                                                                                                                                                                                                                                                                                                                            101pp;
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                                                                                                                                                                                                                                                                                                                                                                English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        healing; periodontal disease; neuronal degeneration.
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2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                      end product receptor are Down's syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand binding site; amyloid-beta; Alzheimer's disease; Down's synd senility; renal failure; hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microglial cell
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13; Conserv
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5.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          periodontal disease, degeneration.
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The present invention describes novel isolated peptides (I) have amino acid sequence corresponding to an amino acid sequence of V-domain of a receptor for an advanced glycation end product (Notes) and the sequence of the s

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC (ABP) interaction with a receptor for RAGE when the receptor is on the CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) clinhibiting formation of an ABP fibril on a cell; (4) inhibiting CC extracellular assembly of an ABP into a fibril; (5) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a CC aggregation of ABP on the surface of a cell; (6) inhibiting activation of a cC cell; (9) evaluating the ability of an agent to inhibit binding of an CC associated with an interaction of an ABP with a receptor for RAGE on a CC cell; (9) evaluating the ability of an agent to inhibit binding of an CC ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a RAGE when the receptor is on the surface of a cell; (2) and (13) treating a subject with a condition associated with an CC with a receptor for RAGE on a scoll. The methods CC and coll treating conditions associated with an interaction of an BAGE with a receptor for RAGE on a cell. The methods CC can be used for treating conditions associated with an interaction of an CC can be used for treating conditions associated with an interaction of an BAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's CC disease, senility, renal failure, hyperlipidaemic atherosclerosis, amyloidosis, an analytimume disease. Inflammation, a tumour cancer male impressed.
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Best Local
                              Claim 2; Page 47; 90pp; English
                                                                                    Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; soluble receptor; advanced glycosylation end product; RAGE; AGE; antibody; vascular permeability; immunologically active fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an autoimmune disease, inflammation, a tumour, cancer, male impotence, wound healing, periodontal disease, neuropathy, retinopathy, nephropathy or neuronal degeneration.
                                                                                                                                           WPI; 1997-558580/51.
                                                                                                                                                                                                                                                     16-APR-1996;
                                                                                                                                                                                                                                                                                       11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human soluble RAGE immunologically active fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW44209 standard; peptide; 10
                                                                   permeability, useful to treat diabetes mellitus
                                                                                                                                                                             Hollander DA, Morser MJ, Nagashima
                                                                                                                                                                                                                 (SCHD ) SCHERING PATENTE AG
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The present sequence represents an immunologically active fragment

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Matches 10
                                                                                                                                                                          of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.
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US-08-685-558A-2

US-08-167-88-2

US-08-173-436A-2

US-08-173-436A-2

US-08-277-231A-4

US-08-277-231A-4

US-08-473-750-7

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Sequence 153, Appli
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1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

Query Match Best Local S Matches

30; Similarity

100.0%; Score 30; ilarity 100.0%; Pred. No. Conservative 0; Mismatch 0;

Mismatches

0;

Gaps

0;

.2e-24;

Length 318; Indels

RESULT 1 US-08-633-148-4 Sequence 4, A Patent No. 58 GENERAL TELE OF I TITLE OF I TITLE OF I TITLE OF I TITLE OF I APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: COUNTER: COUNTER: COUNTER: STATE: COUNTER: COUNTER: COUNTER: FILING D CLASSIFI ATTORNEY/A NAME: W REFERENC TELEPHON TELEPHON TELEPHON TELEPHON TELEPHON SEQUENCE C LENGTH: TYPE: A STRANDEE: WOLECULE I TYPE: A STRANDEE: WOLECULE T TOPOLOGY MOLECULE T	66000000000000000000000000000000000000
8-4 Applicati , Applicati , Applicati 5864018 NT: MORSER NT: MORSER NT: HOLLAN F INVENTION OF SEQUENCE CONDENCE ADEC SAN FRANCE : CALIFORN RY: U.S.A. 94111 SAN FRANCE : CALIFORN RY: D.S.A. 94111 SAN FRANCE : CALIFORN RY: D.S.A. 94111 SAN FRANCE : CALIFORN RY: D.S.A. 94111 SAN FRANCE : TOWN TYPE: FI FER: IBM TYPE: P1 FER: IBM TYPE: P1 TING SYSTEM ARE: PATION NUME G DATE: 11 ARE: PATION MUNICATION HONE: (415) AX: (415)	5 5 6 5 6 5 6 5 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 6 6 6 7 7 7 6 6 6 7 7 7 6 6 6 7 7 7 6 6 6 7 7 7 6 6 6 7
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48 ENT & TOER, & #1.0, 148	US-09-242-131A-1 US-09-615-283-1 US-09-615-283-7 US-08-637-759B-326 US-08-871-355A-326 US-08-637-759B-191 US-08-637-759B-191 US-08-637-759B-191 US-08-637-759B-191 US-09-188-930-153 US-09-188-930-153 US-09-188-930-153 US-09-188-930-23 US-09-085-305-23 US-09-085-305-23 US-09-085-305-23 US-09-085-305-24 US-08-211-202-130 US-08-211-202-140 US-08-211-202-149 US-08-545-809A-91
ADVANCED GLYCOSYLATION CEPTOR POLYPEPTIDES AND USES CREW LLP 8TH FLOOR 005600US	Sequenc Sequenc
S THEREFOR	e 1, Appli e 1, Appli e 7, Appli e 7, Appli e 326, App e 22, Appl e 22, Appl e 21, Appl e 191, App e 193, Appl e 153, Appl e 204, Appl e 27, Appl e 27, Appl e 27, Appl e 27, Appl e 21, Appl

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AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

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                                                                                                                                                                                                   Sequence 5, Apprint No. 5968768
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
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TYPE: a
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TOPOLOGY: li
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                               1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
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: 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                       INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                            Application US/08432016
                                                                    MARQUARDT, HAND
                                                                                                                ARUFFO, ALEJANDRO PATEL, DHAVALKUMAR BOWEN, MICHAEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 amino acids
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 30; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                      HAYNES, BARTON F.
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                                  NIXON & VANDERHYE P.C.
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ER: 014618-005600US
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-432-016-5
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Patent No. 5998172
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/33,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSITUCATION DATA:
PRIOR APPLICATION NUMBER: US 08/333,350
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CD6 LIGAND NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pal-
                               APPLICATION NUMBER: FILING DATE: 18-JU: CLASSIFICATION: 43
                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                  CITY: ARLINGTON
                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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nes 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 01-MA
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22201-4714
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                                                                                                                                                                                                                    VIRGINIA
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                      18-JUL-1996
ON: 435
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 US 08/432,016
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US-08-633-148-18
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                      TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 816-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                           APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE, DOCKET NUMBER: 15'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                  TYPE:
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                 LENGTH: 16 amino acids TYPE: amino acid STRANDEDNESS: single
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linear
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               single
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100.0%; Pr/
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Pred. No.
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-633-148-12
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                                                                          RESULT 7
US-08-633-148-5
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                                              Sequence 5, Application US/08633148 Patent No. 5864018
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                                                                                                                                                                                                   Matches
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Best Local Similarity
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Best Local
   GENERAL INFORMATION:
APPLICANT: MORSER
APPLICANT: NAGASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 16-APR-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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HOLLANDER, DORIS A.
AVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
VENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
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                                                                                                                                                                                                   Conservative
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MORSER, MICHAEL J
NAGASHIMA, MARIKO
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                                                                                                                                                                                                                                                                                                             SS: single
linear
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                                                                                                                                                                                                                  50.0%; Score 15; 100.0%; Pred. No.
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                                                                                                                                                                                                   0;
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7.6e-11;
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MICHAEL J.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICANT: |
APPLICANT: |
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APPLICATION UMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/633,148 FILING DATE: 16-APR-1996
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTIBODIES TITLE OF INVENTION: END-PRODUCT NUMBER OF SEQUENCES: 23
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
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                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sin
TOPOLOGY: linear
CLASSIFICATION:
                                                                                                                                                                                           COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NAGASHIMA, MARIKO
HOLLANDER, DORIS A.
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100.0%; Pred. No.
tive 0; Mismatc
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0.00012;
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Query Match
Best Local Similarity
****hes 6; Conserve
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Best Local Similarity
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                APPLICATION NUMBER: JPA |
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                           MOLECULE TYPE: p
FRAGMENT TYPE: i
ORIGINAL SOURCE:
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/685,558A FILING DATE: 24-JUL-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KITAMURA, NAOMÍ
APPLICANT: MIYAZAWA, KEÍJÍ
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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LENGTH: 10 amino acids
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CITY: Washington
                                                                                                                                                                                                   TOPOLOGY:
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                    10 amino acids
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                                                                                                                                                                  internal fragment
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100.0%;
            20.0%; Score 6; DB ... 100.0%; Pred. No. 2. ... tive 0; Mismatches
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Pred. No.
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                               DB 4;
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                                             Length 10;
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US-08-173-436A-2
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; MOLECULE TYPE: protein
US-08-416-788-2
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US-08-416-788-2
                                                                                                                       Sequence 2, Application US/08173436A Patent No. 5698444
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                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (610)454-380 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING LATE.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/FR93/01012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
              APPLICANT: Baez, Melvyn
APPLICANT: Kursar, Jonathon D.
TITLE OF INVENTION: SEROTONIN RECEPTOR PROTEIN AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/FR93, FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92-12280
FILING DATE: 14-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                253 KPPQRL 258
                                                                                                                                                                                                                                                                22 KPPQRL 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, Julie K. REGISTRATION NUMBER: 38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Collegeville
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19426-0107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Rhone-Poulenc Rorer Inc. 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maroteaux,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (610)454-3808
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 5780245el Polypeptides Having a Serotonin
Receptor Activity, Nucleic Acids Coding for These
Polypeptides and Uses
9
                                                                                                                                                                                                                                                                                                 20.0%; Score 6;
100.0%; Pred. No
Live 0; Mismat
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                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                   Length 479;
                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEFAX: 317-276-3861
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 481 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, PAUL J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 KPPQRL 259
                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 23-DEC CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Lilly Corpo
CITY: Indianapolis
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 KPPQRL 27
                                                FILING DATE:
                                                                 APPLICATION NUMBER:
                                                                                                                FILING DATE:
                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
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amino acid

amino acid

OGY: linear
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NVENTION: NOVEL HISTAMINE H2 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                        Guegler, Karl J.
Goli, Surya K.
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N: 435
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   36,749
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Pred. No
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52;
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Query Match
Best Local Similarity
----hes 6; Conserve
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US-08-685-558A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08685558A Pattent No. 6225081
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                                                                                                                                                                                                                                      APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-UUL-1995
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 475198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 KPPQRL 259
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/685,558A FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         ORGANISM:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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MIYAZAWA, Keiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenBank
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                Conservative
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100.0%; FI
           20.0%; Score 6; DB / 100.0%; Pred. No. 54. tive 0; Mismatches
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                             DB 4;
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o. 52;
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                                          Length 513;
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             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-277-231A-4
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US-08-277-231A-4
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                                                         Patent No. 5834187
Patent No. 5834187 5786143
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Patent NO. 5643725
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Applic Patent No. 5643725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 861-62.
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO:
         TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. 5834187 5786
TITLE OF INVENTION: Haemophilus Influenzae
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acids
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TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                     157 TARIGE 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/277,231A FILING DATE: 19-JUL-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                   5 TARIGE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Carroll, Alice O. REGISTRATION NUMBER: 32
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Brinton, Charles C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus Influenzae
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                 DB 1;
o. 74;
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GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton Jr., Charles C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and Analysis of LKP Pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural Genes and The LKP Pili Operon of No. 5643725typa
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

217: 02173

COMPUTER RADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: BATCHIN Release #1.0, Version #1.30

COURTON NUMBER: US/08/473,750

FILING DATE: 07-UN-1995

CLASSIFICATION NUMBER: US/08/473,750

FILING DATE: 07-UN-1995

CLASSIFICATION NUMBER: US/08/473,750

FILING DATE: 07-UN-1995

CLASSIFICATION NUMBER: US/08/277,321

FILING DATE: 19-UN-1994

ATTORNEY/ACENT INFORMATION:

APPLICATION NUMBER: US/08/277,321

FILING DATE: 19-UN-1994

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 741 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: molicody: linear

NOLSCULE TYPE: protein

US-08-473-750-7

Ouery Match

MEDIUM TYPE: protein

Ouery Match

Septime Type: protein

Ouery Match

Septi
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Total number of hits satisfying chosen parameters:
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                                                                              Searched:
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Perfect score:
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                                                                                                                  OLIGO Gapop 60.0 , Gapext 60.0
                                                                            219241 seqs,
                                                                                                                                                                                                                                                                                             April 24, 2002, 09:23:16;
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                                                                                                                                                                          AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 (c) 1993 - 2000 Comp
                                                                              76174552 residues
                                                                                                                                                                                                                                                                                             Search time 38.65 Seconds
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59.126 Million cell updates/sec
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and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution. Minimum Maximum

DB seq

length: 0 length: 2000000000

Database :

PIR\_68:\*

Post-processing: Listing first 45 summaries

#### SUMMARIES

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I38423	BABOH	S54505	A70983	E71733	G84832	C83322	A84748	T24462	T05278	T05671	JE0312	T36710	S27269	S49442	S43687
aspartyl beta-hydi	peptide-aspartate	hypothetical prote	probable fusA2 pro	threoninetRNA 1:	ATP-dependent RNA	excinuclease ABC s	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	3-ketosteroid-deta	hypothetical prote	serotonin receptor	serotonin recepton	serotonin recepton

#### ALIGNMENTS

A; Reference number: A55562; MUID:95137587 A; Accession: I61596 A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/	Genomics 23, 408-419, 1994  A; Title: Three genes in the human MHC class III region near the junction with the cla	C;Species: Homo sapiens (man) C;Date: 24-May-1996 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999 C;Accession: I61596; B42879; S27968 R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko,	RESULT 1 I61596 advanced glycosylation end-products receptor precursor – human N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot

A; Molecule type: DNA A; Residues: 1-404 < RES> inslated from GB/

A;Cross-references: GB:D28769; NID:g561657; PIDN:BAA05958.1; PID:g561659
R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation A;Reference number: A42879; MUID:92340547
A;Accession: B42879.

A; Molecule type: mRNA

A;Residues: 'G',2-99,'R',101-404 <NEE>
A;Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846
A;Experimental source: lung

A; Note: sequence extracted from NCBI backbone (NCBIP:109438)

C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly cellular function, thus contributing to tissue lesions in diabetes. C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

C; Genetics: A; Gene: GDB: AGER

A;Cross-references: GDB:306354; OMIM:600214
A;Map position: 6p21.3-6p21.3
A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2

A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C; Function:

C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG> F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT F;23-344/Domain: extracellular #status predicted <EXT> F;31-101/Domain: immunoglobulin homology <IM1>

F:137-210/Domain: immunoglobulin homology <IM2>
F:252-303/Domain: immunoglobulin homology <IM3>
F:365-302/Domain: transmembrane #status predicted <TMM>
F:363-404/Domain: intracellular #status predicted <IMY>
F:25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted F:38-99,144-208,259-301/Disulfide bonds: #status predicted

the neurotoxic pathway that produces dementia in Alzheimer's disease

ng protein involved immunoglobulin homo

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A; Molecule type: DNA
A; Residues: 1-402 <ROW>
A; Cross-references: EMBL: AF030001; NID: g2564945; PID: c; Genetics:
A; Gene: RAGE
A; Map position: 17
A; Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 277
C; Superfamily: advanced glycosylation end products rec C; Keywords: receptor; transmembrane protein
F; 31-100/Domain: immunoglobulin homology <IMM>
A;Cross-references: GB:M91212; NID:g163650; PIDN:AAA03575.1; PID:g163651
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
A;Note: parts of this sequence, including the amino end of the mature protein, C.; He
J; Biol. Chem. 267, 14987-14997, 1992
A;Pitle: Isolation and characterization of two binding proteins for advanced glycosylati
A;Reference number: A42878; MUID:92340546
A;Reference number: A42878; MUID:92340546
A;Residues: 23-24, X; 26-37, X; 39-49, XX', 52-54 <SCH>
A;Residues: 23-24, X; 26-37, X; 39-49, XX', 52-54 <SCH>
A;Residues: 23-24, X; 26-37, X; 39-49, XX', 52-54 <SCH>
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)
C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosylation function, thus contributing to tissue lesions in diabetes.
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            advanced glycosylation end-products receptor precursor - bovine N.Alternate names: advanced glycosylation end product-binding protein, 35K; C;Species: Bos primigenius taurus (cattle) C;Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999 C;Accession: A42879; A42878; S27949 R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ell J. BBiol. Chem. 267, 14998-15004, 1992 A;Title: Cloning and expression of a cell surface receptor for advanced gly A;Reference number: A42879; MUID:92340547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: RAGE
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C;Accession: T09062
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09062
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A; Residues: 1-416 <NEE>
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A; Accession: A42879
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. 5.2e-06;
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                                                                 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUID:20222556 A;Accession: E81998
                                                                                                                                                                                                                                                            pseudouridylate synthase (EC 4.2.1.70) C rRNA-specific NMA0070 (imported) -
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
           A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                  R;Parkhill, J.; Achtman, M.; James, ; Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
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S.R.; Mo Rajandre

Neisseria

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A; Gene: mutH
C; Superfamily: mutator mutH
                                                                                                                                                                                                                                                                                                                           A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; SA;Title: Whole-genome random sequencing and assembly of Haemophilus A;Reference number: A64000; MUID:95350630
A;Accession: H64065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: DNA mismatch proteir C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;355-372/Domain: transmembrane #status predicted <TMM>F;357-372/Domain: intracellular #status predicted <INT>F;275.80/Binding site: carbohydrate (Asn) (covalent) #status F;38-98,143-207,269-311/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;23-354/Domain: extracellular #status predicted <EXT>
F;31-100/Domain: immunoglobulin homology <IM1>
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                                    QΥ
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F;262-313/Domain: immunoglobulin homology <IM3>
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A; Residues: 1-223 <TIGR>
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100.0%;
                                                                                                    23.3%;
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Pred. No.
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(covalent) #status
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A; Cross-references: GB:AL162752;

A; Residues: 1-330 < PAR>

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A;Gene: F
C;Superfamily: cell fusion glycoprotein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F:23-101/Product: cell fusion glycoprotein F2 #status predicted
                                                                                                                                                                                                       J. Gen. Virol. 73, 1717-1724, 1992
A;Title: Sequence analysis of the gene encoding A;Reference number: JQ1619; MUID:92333256
A;Accession: JQ1619
A;Moleculo ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: rluC; NMA0070
C;Superfamily: conserved hypothetical protein HI0176
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                      cell fusion glycoprotein precursor - pneumonia virus of mice N,Alternate names: F protein N;Contains: cell fusion glycoprotein F1; cell fusion glycoprotein C;Species: pneumonia virus of mice C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
H81225
                                                                                                                                     A;Cross-references: GB:S40186 C;Genetics:
                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-537 < CHA>
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R; Chambers, P.;
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C;Superfamily: conserved hypothetical protein HI0176
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A; Residues: 1-330 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755
A;Accession: H81225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: H81225
R; Tettelin, H.; Sau
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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100.0%;
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A, strain Z2491
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0; Mismatches
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                                                                                                                                                                                                                                                        the fusion glycoprotein of pneumonia vi
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strain MC58.
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, F. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MUID:21016719
A;Actression: B86212
                                                                                                                                                     A; Note: root-specific
C; Superfamily: cystatin;
C; Keywords: cysteine prot
                                                                                                                                                                                                                                                                                                                                                  A;Description: Cystein proteinase inhibitor.
A;Reference number: 216154
A;Accession: T07822
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cystein proteinase inhibitor - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein F24B9.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86212
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                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-96 < YAM>
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A; Residues: 1-595
                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AB014760; PIDN:BAA28867.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yamakawa,
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Best Local :
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Similarity 6; Conserv
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teinase inhibitor
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                   DB .
26;
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11;
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                                                           Length 96;
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Maiti, R.;
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Conservative

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hypothetical protein Rv0804 - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis c;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-C;Accession: E70536 R;Gole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
$64538
hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae)
hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G7821
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
C;Accession: $64538
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46154
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselenbeitted to the Protein Sequence Database, December 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z73000; NID:g1323386; PID:g1323387; GSPDB:GN00007; MIPS:YGR215vA;Experimental source: strain S288C C;Genetics:
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A; Residues: 1-155 < NYA>
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A; Accession: T46154
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C;Superfamily: Saccharomyces cerevisiae hypothetical
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A; Introns: 118/3
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A; Residues: 1-110 <RIE>
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A; Accession: S64538
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Best Local S
Matches 6
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les 6; Conserv
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LVLKCK 64
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100.0%; Pr
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Mismatches
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                                                                                                                                                                                                                                                                                                      DB
39;
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29;
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                                         #text_change 22-Oct-1999
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  C.; Harris, D.;
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  Gordon,
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:
                                                                                                                                                                     membrane antigen gp85 - human herpesvirus 4 (strain B95-8) C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_c C;Accession: F43044; A03787; S33040 R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, Mol. Biol. Med. 1, 21-45, 1983
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24835.1; PID:g1334899 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; G:Nature 310, 207-211, 1984
                                                                                                         A;Title: Sequence analysis of the 17,166 A;Reference number: A93065; MUID:85035713 A;Accession: F43044
                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                A; Molecule type: DNA
A; Residues: 1-234 <BAN>
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EcoRI fragment C of

B95-8 Epstein-Barr vi

Gibson,

T.J.

Barrell, B

#text\_change 16-Jul-1999

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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: E70536
A;Status: preliminary; nucleic acid sequence not s
                                             Query Match
Best Local Similarity
""" 6; Conservi
                                                                                                                                                                                                                                                                                                C;Accession: A75260

R;White, O.; Eisen, J.A.; Heidelberg, J.F.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresista
A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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Best Local Similarity
""+ hes 6; Conserv:
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A; Residues: 1-209 <COL>
A; Cross-references: GB: Z95618;
A; Experimental source: strain F
C; Genetics:
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121 ARIGEP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GEPLVL
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                             6 ARIGEP
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                                                               Conservative
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                                                                 0;
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                                                                               Score 6;
Pred. No.
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53;
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49;
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tuberculosis fi
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, L.; Utterback, T.; Z:
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                                                                                                                                                                                                                                                                                                                       Deinococcus radiodurans
                                                                                                                                                                                                                   PIDN: AAF12096.1;
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RESULT 15
H64181
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A;Cross-references: GB:L42023; TIGR:HI1079
C;Superfamily: histidine permease protein M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, I. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
A;Accession: H64181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667
A;Contents: annotation; protein coding region
C;Superfamily: Epstein-Barr virus membrane antigen gp85
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Search completed: April 24, 2002, 09:23:17 Job time: 246 sec
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Aug-1998
C;Accession: H64181
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.0%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches
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100.0%; Pred. No. 55
tive 0; Mismatches
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Result
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Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB DB
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AAY09349
AAY52134
AAW44200
AAW33754
AAY52130
AAW33753
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AAW33753
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                                                                                                                                                                                                                                                                                       SUMMARIES
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33.527 Million cell updates/sec
                                                   Human mature recep
Human RAGE polypep
Human Receptor to
Human soluble rece
Human RAGE polypep
Extracorporeal cir
                                                                                                                                                                                                                            Description
                 Extracorporeal cir
Mouse RAGE V-domai
Bovine RAGE V-doma
                                                                                                                                                                      Human
                                                                                                                                                                                          Human
                                                                                                                                                                    RAGE V-domai
Receptor to
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45	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
52	52	ъ	52	52	52	52	52	52	52	52	52	52	52.5	53	53	53	53	53.5	ω	54	54	55	55.5	5	60	60	60	60	72	72	81	81	127
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312	312	312	312	312	312	312	312	303	298	298	298	298	4412	1651	1649	753	298	1101	767	602	602	312	1496	1496	10	10	10	10	15	15	16	16	30
22	22	21	21	21	20	20	20	22	22	21	21	19	21	20	20	20	19	20	22	18	15	22	21	20	18	18	18	18	18	18	18	18	18
AAU00821	AAU12339	AAY70668	AAB24401	AAB33421	AAY13354	AAY23324	AAY08060	AAM23693	AAU00512	AAB27275	AAB27273	AAW85457	AAY53666	AAY13566	AAY08404	AAW83927	AAW75220	AAY08008	AAM25696	AAW32900	AAR51705	AAB50904	AAY70469	AAW81030	AAW33755	AAW33763	AAW44201	0	37	420	376	42	AAW23337
Human immune respo				PRO245	acid :	A33 related antige	n PRO24:	Human EST encoded		⋖	fluency	Secreted protein e	Sequence qi/101742	Human Robo 1 polyp	Human ROBOI protei	Human T85 protein.	Human secreted pro	HLIG-1 p	Human protein sequ	0	trophic	PRO24	+	oma as	RAGE polype	RAGE polype		Human soluble RAGE	Human RAGE polypep	Human soluble RAGE	RAGE	Human soluble RAGE	N-terminal sequenc

### ALIGNMENTS

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RESULT
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                                                                                                                                                                                                        RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's synd senility; renal failure; hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
           WPI; 1999-277439/23
                                                                                   09-OCT-1997;
                                                                                                           09-OCT-1998;
                                                                                                                                                                                                                                                                                                            Human RAGE V-domain peptide SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                     09-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 AAY09349;
                                                          (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                    22-APR-1999.
                                                                                                                                                           WO9918987-A1.
                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      AAY09349 standard; peptide; 30
                                   Lamster I,
                                                                                                                                                                                                                                                                                                                                                                                                                ...
                                   Schmidt AM,
                                                                                   97US-0948131.
                                                                                                           98WO-US21346
                                  Stern D,
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                                   Yan
                                   SD;
                                                                                                                                                                                                                                                           own's syndrome; dementia;
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Rat RAGE

V-domain

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RESULT
AAY52134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting (CC extracellular assembly of an ABP into a fibril; (5) inhibiting infiltration aggregation of ABP on the surface of a cell; (6) inhibiting infiltration confidence of a cell; (6) inhibiting infiltration confidence in the surface of a cell; (6) inhibiting activation of a microglial cell into senile plaques; (7) inhibiting activation of a microglial cell by an ABP; (8) treating a subject with a condition consisted with an interaction of an ABP with a receptor for RAGE on a cell; (9) evaluating the ability of an agent to inhibit binding of an cell; (9) evaluating the ability of an agent to inhibit binding of an cell; (10) condition of a NF-kappaB gene in a cell; (11) inhibiting condition of a NF-kappaB gene in a cell; (11) inhibiting condition of a NF-kappaB gene in a cell; (11) inhibiting condition associated with an interaction of an cell; (12) inhibiting an cell; (13) treating a subject with a condition associated with an interaction of an cell; (13) treating conditions associated with an interaction of an CC interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an CC abBP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's centurinal cytotoxicity, Down's syndrome, dementia associated with head converted the condition and condition associated with head converted disease, inflammation, a tumour, cancer, male impotence, correctly and conditional disease, neuropathy, retinopathy, nephropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                             Soluble receptor for advanced glycation endproducts; RAGE; tumour; invasion; metastasis; amphoterin; neuron; inhibit; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Also described are methods for: (1) inhibiting an amyloid-beta peptide (ABP) interaction with a receptor for RAGE when the receptor is on the surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
WPI; 2000-013260/01
                                    Schmidt AM,
                                                                                                                   17-APR-1998;
                                                                                                                                                       16-APR-1999;
                                                                                                                                                                                              28-OCT-1999
                                                                                                                                                                                                                                  W09954485-A1
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Human Receptor
                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides based on an advanced glycation end product receptor are useful for treating Alzheimer's disease and Down's syndrome
                                                                          (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52134 standard; protein; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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f a receptor for an advance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                    Stern D
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                   98US-0062365
                                                                                                                                                       99WO-US08427
                                                                                                                                                                                                                                                                                                                                                                        AGE (RAGE) amino acid sequence fragment #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribes novel isolated peptides (I) ponding to an amino acid sequence an advanced glycation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 162; DB 20;
Pred. No. 2.5e-15;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product (RAGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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RESULT
AAW44200
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts was range of physiologically and pathophysiologically relevant ligands
                                         Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular
                                                                                                WPI; 1997-558580/51.
                                                                                                                                                                                                                                                                      WO9739125-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            Human mature receptor to an advanced glycosylation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 29; Page 62;
                        permeability, useful
                                                                                  N-PSDB; AAV12395
                                                                                                                                                                                  16-APR-1996;
                                                                                                                                                                                                              11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting tumour invasion or spreading by administration of soluble
                                                                                                                           Hollander DA,
                                                                                                                                                       (SCHD ) SCHERING PATENTE AG
                                                                                                                                                                                                                                          23-OCT-1997.
                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                  antibody;
                                                                                                                                                                                                                                                                                                                                                                                                soluble
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                                                                                                                                                                                                                                                                                                                                                                                  receptor; advanced glycosylation end product; RAGE; vascular permeability; diabetes mellitus.
                                                                                                                            Morser
                                                                                                                                                                                  96US-0633148
                                                                                                                                                                                                              97WO-EP01834
                                                                                                                                                                                                                                                                                                               Location/Qualifiers 66
                                                                                                                                                                                                                                                                                                  /note= "encoded by CCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                           ξ
                                                                                                                           MJ,
                           treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                           Nagashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 162; DB 21;
Pred. No. 2.5e-15;
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0;

Claim 2; Page 42-43; 90pp; English.

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RESULT
AAW33754
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Best Local
                                                                                                                           This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (318 amino acid residues). The RAGE polypeptides and its active fragments or their mimetics, inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). The are used to treat diseases associated with AGE/RAGE interaction, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Advanced glycosylation vascular permeability; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular
                         disorders such as neuropathy, nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated amyloidosis,
                                                                                                                                                                                                                                                                                                      Claim 3;
                                                                                                                                                                                                                                                                                                                                                   New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-526458/48.
N-PSDB; AAV06518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
  of microglial
                                                                           increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHD ) SCHERING AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosylation end-product receptor; RAGE; screening; AGE; permeability; diabetes mellitus; treatment; atherosclerosis; r's disease.
                                                                                                                                                                                                                                                                                                 Fig 1B; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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  cells by
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Pred. No. 2.7
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.7e-14;
s 0;
Alzheimer's disease or
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                         also activation
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                           considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but
                                                                                                                                                                                     This is the amino acid sequence of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with a range physiologically and pathophysiologically relevant ligands when
                                                                                                                                                                                                                                                                                                                         WPI;
                                       amount of the pharmaceutical composition containing a RAGE polyper
The invention also relates to a method for evaluating the ability
agent to inhibit tumour invasion in a local cellular environment.
                                                                                  both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective invasion and metastasis via administration of a therapeutically effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes.
                           can be administered
                                                                                                                                                                                                                                                 Disclosure; Page 10-11;
                                                                                                                                                                                                                                                                                          Inhibiting
                                                                                                                                                                                                                                                                                                                                                    Schmidt AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble receptor for advanced glycation endproducts; RAGE; tumour;
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                                                                                                                                                                                                                                                                                          tumour invasion or spreading by administration of soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                              88pp;
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                           patient in a pharmaceutically acceptable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Pred. No.
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.7e-14;
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Matches 30
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, haemodialysis associated amyloidosis or atheroselerosis. The Ab can also be used for the collection of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 40-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; soluble receptor; advanced glycosylation end product; RAGE; AGE; antibody; vascular permeability; diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                              the isolation and purification of human RAGE polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHD ) SCHERING PATENTE AG
   23
                                      1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK
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                                                                                                                                                                                                                                                                                                                                             340 AA
                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagashima M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340
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                                                                                                                                                   0;
                                                                                                                                                                                      Score 162; DB 18;
Pred. No. 2.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                         30
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                                                                                                                                                                                                                 Length
                                                                                                                                                   Indels
                                                                                                                                                                                                                        340;
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AAB81925 ID AAB8

AAB81925 standard; protein; 404 AA.

RESULT

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Db Qy

23

1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

aqnitarigeplylkckgapkkppqrlewk 52

Query Match Best Local ( Matches 3)

Local Similarity hes 30; Conserv

100.0%; ilarity 100.0%; Conservative (

0;

Score 162; | Pred. No. 2.; Mismatches

; DB 18; 2.9e-14;

Length Indels

340;

Gaps

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RESULT
AAW33753
disorders such as neuropathy, nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                                                                                        glycosylation end products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular commandation.
                                                                                                                                                                                                                                                                                                                                                                 This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (340 amino acid residues). The RAGE polypeptides and its polypeptide (advantage) active fragments or their mimetics, inhibit interaction between advantage of the polypeptides and the polypeptides are the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Advanced glycosylation end-product receptor; vascular permeability; diabetes mellitus; translatheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW33753 standard; Protein;
Sequence
                                      genes.
                                                                                                                                                                                                                                                                                          increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1A; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-526458/48
N-PSDB; AAV06517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09739121-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human RAGE polypeptide (340 amino acid residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHD ) SCHERING AG
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340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAGE; screening; AGE;
eatment; atherosclerosis;
                                                                                                                                                                                                                                                                                              or occlusive vascular
                                                                                                                                                                                                                                                                                                                                   AGE). They such as
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                                                                                                                                                                                                                             RESULT
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Best Local
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                                                           ligand binding site; amyloid-beta; Alzheimer's disease; Desenility; renal failure; hyperlipidaemic atherosclerosis; neuronal cytotoxicity; head trauma; amyotrophic lateral so
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a material for extracorporeal circulation which is made from a water-insoluble carrier immobilized with a protein having the sequence shown here. The materials of the invention, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracorporeal circulation; carbonyl stress product; receptor;
  Mus sp
                                                                                                                                                   09-JUL-1999
                                                                                                                                                                            AAY09350;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               fluid, and are therefore useful in treating vascular lesions arteriosclerosis due to carbonyl stress products caused by ab
                                                                                                                                                                                                                                                                                                                                                                                                                                       adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dysfunction in vascular lesions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracorporeal circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB81925;
                         neuropathy;
                                      tumour;
                                               multiple sclerosis;
                                                                                                                          Mouse
                                                                                                                                                                                                    AAY09350 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    promoted carbonyl stress from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                        1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK
                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                              2001-290314/30.
                                                                                                  V-domain; receptor for advanced glycation endproduct;
                                                                                                                         RAGE V-domain peptide SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                  30;
                                      cancer; male
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 31-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vascular
                                                                                                                                                                                                                                                                                                                                                                              404
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-JP06172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lesion; excretory dysfunction
                                                                                                                                                                                                  peptide;
                                    ty; head trauma; amyotrophic lateral sclerosis;
amyloidosis; autoimmune disease; inflammation;
e impotence; wound healing; periodontal disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akiyama
                                                                                                                                                                                                                                                                                                                           .0%;
                         nephropathy; neuronal degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         material receptor protein
                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                     excretory
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                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                           162;
No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                     dysfunction.
                                                                                                                                                                                                                                                                                                                          DB 22;
}.4e-14;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                       Length
                                                                                     Down's syndrome;
                                                                                                                                                                                                                                                                                                                                        404;
                                                                         dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                 abnormally
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                Gaps
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KW XXX DXXX ACX XXX
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                                                                                                                                                                                                                            AAY09352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC (ABP) interaction with a receptor for RAGE when the receptor is on the CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting CC extracellular assembly of an ABP into a fibril; (5) inhibiting CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a microglial cell by an ABP; (8) treating a subject with a condition of a sesociated with an interaction of an ABP with a receptor for RAGE on a CC cell; (9) evaluating the ability of an agent to inhibit binding of an CC alsociated with a v-domain of a receptor for RAGE on the surface of a cell; (10) CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction of with a receptor for RAGE on the surface of a cell; CC and (13) treating a subject with a condition associated with an CC interaction of an RAGE with a receptor for RAGE on a cell. The methods CC can be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods CC can be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's CC disease, senility, renal failure, hyperlipidaemic atheroscierosis, anyloidosis, anyl
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequence corresponding to an amino acid sequence of a V-domain of a receptor for an advanced glycation end product (RAGE). Also described are methods for: (1) inhibiting an amyloid-beta peptide
                                                                                                                         09-JUL-1999
                                                                                                                                                                  AAY09352
                                                                                                                                                                                                        AAY09352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an autoimmune disease, inflammation, a tumour, cancer, male impotence, wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1997;
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                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                     2 QNITARIGEPLVLKCKGAPKKPPQRLEWK 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptides based on
                                                                                                                                                                                                                                                                                                          qnitarigeplylsckgapkkppqqlewk
                                                                               RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tor
                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          es based on an advanced glycation treating Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
                                                                             V-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLUMBIA NEW YORK.
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                                                                                                                                                                                                      peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%;
93.1%;
                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                           30
                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                               Score 149; DB 20;
Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                             IJ
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                                                                               NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated peptides (I) an amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end product receptor Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 30
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of a
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's senility; renal failure; hyperlipidaemic atherosclerosis; demer

own's syndrome; dementia;

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AAY09351
ID AAY(
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AC AAY(
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DT 09-;
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                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes novel isolated peptides (I) having an CC amino acid sequence corresponding to an amino acid sequence of a CC v-domain of a receptor for an advanced glycation end product (RAGE). CC Also described are methods for: (1) inhibiting an amyloid-beta peptide (C (ABP) interaction with a receptor for RAGE when the receptor is on the CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) inhibiting formation of an ABP fibril on a cell; (4) inhibiting cell into senile plaques; (7) inhibiting infiltration of a gargegation of ABP on the surface of a cell; (5) inhibiting activation of a microglial cell into senile plaques; (7) inhibiting activation of a microglial cell by an ABP; (8) treating a subject with a condition cassociated with an interaction of an ABP with a receptor for RAGE on a cell; (10) evaluating the ability of an agent to inhibit binding of an ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10) cell in a cell into senile plaques; (7) inhibiting an the cell; (10) cell in a cell into senile plaques; (7) inhibiting an activation of an ABP with a receptor for RAGE on the surface of a cell; (10) cell in a cell into a cell into senile plaques; (7) inhibiting an RAGE interaction of an RAGE with a subject with a cendition associated with an interaction of cell interaction of an RAGE with a receptor for RAGE on a cell. The methods cell interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an BBP or an RAGE with a receptor for RAGE on a cell interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell interaction of an CC and cytotoxicity, Down's syndrome, dementia associated with head conditions and anyotrophic lateral sclerosis, multiple sclerosis, amyloidosis, an unital disease. Inflammation, a tumour cancer.
                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                    Matches
  09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
                                             AAY09351;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-277439/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                   AAY09351 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; inflammation, a tumour, cancer, male impotence, und healing, periodontal disease, neuropathy, retinopathy, nephropat neuronal degeneration.
                                                                                                                                                                                               N
                                                                                                                                                                                                                                       2 QNITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptides based on an advanced glycation end product receptor are ful for treating Alzheimer's disease and Down's syndrome
                                                                                                                                                                                             qnitarigkplvlnckgapkkppqqlewk 30
                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                  Similarity 89.
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              30
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  (first entry)
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                                                                                   peptide;
                                                                                                                                                                                                                                                                                                    89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stern
                                                                                       30
                                                                                                                                                                                                                                                                                  ?,
                                                                                                                                                                                                                                                                                                      Score 145;
Pred. No. 5
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                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                    DB 20;
.2e-13;
                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                           Length 30;
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2 QNITARIGEPLVLKCKGAPKKPPQRLEWK 30

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CC (ABP) interaction with a receptor for RAGE when the receptor is on the curriace of a cell; (2) inhibiting degeneration of a neuronal cell; (3) cc inhibiting formation of an ABP ilbri on a cell; (4) inhibiting cc extracellular assembly of an ABP into a fibril; (5) inhibiting infiltration of aggregation of ABP on the surface of a cell; (6) inhibiting activation of a microglial cell by an ABP; (8) treating a subject with a condition cc associated with an interaction of an ABP with a receptor for RAGE on a cell; (9) evaluating the ability of an agent to inhibit binding of an CC eal; (9) evaluating the ability of an agent to inhibit binding of an CC aBP with a v-domain of a receptor for RAGE on the surface of a cell; (10) cl inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting condition associated with an receptor for RAGE when the receptor is on the surface of a cell; (10) cl interaction of an RAGE with a condition associated with an ccl interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's conserved and contact of its associated with head contained mune disease, inflammation, a tumour cancer male importance.
                  Query Match
Best Local
    Matches
                                                                                                                                          or neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzhelmer's disease; Down's synd senility; renal failure, hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; canoer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V-domain of a receptor for an advanced glycation end product (RAGE). Also described are methods for: (1) inhibiting an amyloid-beta peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes novel isolated peptides (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 78; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides based on an advanced glycation end product receptor are useful for treating Alzheimer's disease and Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1998;
                                                                                                  Sequence
                                                                                                                                                                                  an autoimmune disease, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9918987-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat RAGE V-domain peptide SEQ
                                                                                                                                          and healing, periodontal disease, neuropathy, retinopathy, nephropathy neuronal degeneration.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence corresponding to an amino acid
                                                                                                  30
                                                                                                    A
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                  82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stern D,
                  Score 133;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:3
  Mismatches
                                                                                                                                                                                  a tumour, cancer, male impotence,
                  DB 20;
2.2e-11;
                                     Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Down's syndrome;
0;
Gaps
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AAW23337 standard; peptide;

30

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2 qxitarigkplvlnxkgapkkppqqlewk 30

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δõ
                                                                                                                                                                                                                     CC outgrowth, generate reactive oxygen intermediates, induce cellular considers tress, lead to neuronal cytotoxcity, and promote microglial cactivation. The 50 kDa protein was purified from rat epthelial cells and cis shown to be virtually identical to a bovine receptor for the advanced glycosylation end product. Peptides derived from the amyloid beta cepturises an agent capable of inhibiting interaction. This composition comprises an agent capable of inhibiting interaction of an amyloid beta cepturises an agent capable of inhibiting interaction of anyloid beta comprises an agent capable of carrier. A method for inhibiting interaction on the surface of a cell comprises contacting the cell with e.g. present peptide. Depending on the type of cell, inhibiting the interaction between the amyloid beta peptide of amyloid beta peptide fibril on a cell, inhibiting aggregation of an amyloid beta peptide into a fibril, inhibiting aggregation of a cell, inhibiting aggregation of a cell, inhibiting aggregation of a cell, inhibiting activation of an incroglial cells by amyloid beta peptide. The methods can be used for treating e.g. diabetes, Alzheimer's Disease, senility, renal failure, cellement associated with head tranna. amyotorbic lateral scherars of a cell admonstration of a cell with the methods can be used for the cells by admit a stranger of a cell, inhibiting activation of a cell with head tranna. amyotrobic lateral scherars of a cell chements as colated with head tranna. amyotrobic lateral scherars of a cell chements.
                                                         Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal of a 50 kDa cell-associated protein which binds the amyloid beta peptide. This peptide is the principal component of extracellular deposits in Alzheimer's disease. It has been shown to promote nuerite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amyloid beta peptide fibril
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the amino acid sequence of the N-terminal of a 50 kDa cell-associated protein which binds the amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting damage to cells in e.g. Alzheimer's disease - using an agent which inhibits interaction of an amyloid-beta peptide with a receptor for advanced glycosylation end product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-393374/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmidt AM, Stern D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor for advanced glycosylation end product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nuerite outgrowth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal sequence of a protein which binds the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23337;
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                      N
                    QNITARIGEPLVLKCKGAPKKPPQRLEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) UNIV COLUMBIA NEW YORK
                                                                           Similarity
                                                                                                                                                                                                             associated with head trauma, amyotrophic lateral sclerosis,
                                                                                                                                                                                               sclerosis
                                                                                                                                                        30
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; extracellular deposit; Alzheimer's
rowth; microglial activation; neuronal cell d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US00857
                                                                                                                                                                                           or neuronal degeneration.
78.4%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yan SD;
                                                         2;
                                                                           Score 127;
Pred. No. 1
                                                         Mismatches
                                                                           DB 18;
                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amyloid beta peptide
                                                                                           Length 30;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degeneration;
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                                                      Gaps
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AAW33768
ID AAW3
XX
AC AAW3
XX
DT 08-P
                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (RAGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculapathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; soluble receptor; advanced glycosylation end product;
AGE; antibody; vascular permeability; immunologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human soluble RAGE immunologically active fragment SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW44214 standard; peptide; 16 AA.
                                                               AAW33768;
                                                                                                        AAW33768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an immunologically active fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        permeability, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hollander DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCHD ) SCHERING PATENTE AG.
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                                                                                                                                                                                                                                                           1 AQNITARIGEPLVLKC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Page 49; 90pp; English
                                                                                                                                                                                                                                                                                                        Similarity
16; Conser
                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morser MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-EP01834
                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                            .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagashima
                                                                                                          16
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                          Score 81;
Pred. No.
                                                                                                          AA
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                        DB 18;
0.00015;
                                                                                                                                                                                                                                                                                                                                              Length 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active fragment;
                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      0;
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Вþ Qy

08-MAY-1998

(first entry)

Human

RAGE polypeptide

fragment 14

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RESULT 15
AAW44208
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                                                                                                                                                                                                                                                                                                                                                                                              CC This is a peptide fragment of a human advanced glycosylation end-product CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active CC fragments or their mimetics can inhibit interaction between advanced CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They care used to treat diseases associated with AGE/RAGE interaction, such as CC increased vascular permeability, diabetes mellitus (particularly CC complications such as micro- vasculopathy or occlusive vascular CC disorders such as neuropathy, nephropathy, atherosclerosis or CC retinopathy) or haemodialysis-associated amyloidosis, also activation CC age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and CC to screen for compounds that are agonists and antagonists of AGE/RAGE communoassay reagents for measurement of RAGE levels, and as inhibitors of CC interaction between AGE and RAGE or other receptors and for purification CC used to express recombinant RAGE and as probes for isolating related CC denes.
                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
Human; soluble receptor; advanced glycosylation end product; RAGE;
AGE; antibody; vascular permeability; immunologically active fragment;
                                                                              14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Advanced glycosylation vascular permeability;
                                            Human soluble RAGE immunologically active fragment SEQ ID NO:12.
                                                                                                            AAW44208
                                                                                                                                         AAW44208 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                         genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-526458/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morser MJ,
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16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end-product receptor; RAGE; screening; AGE;
diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                         15
                                                                                                                                                                                                                                                                                              Score 81;
Pred. No.
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0.00015;
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Best Local Similarity
Matches 15; Conser
                                                                                                                                                                            of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. maicrovasculopathy, baemodialysis associated amyloidosis or atherosetierosis. The Ab can also be used for associated amyloidosis or atherosetierosis. The Ab can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                       Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                               The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 46; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-558580/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hollander DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCHD ) SCHERING PATENTE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1997
                                                                                                                                                                  the isolation and purification of human RAGE polypeptide.
               1 AQNITARIGEPLVLK 15
l aqnitarigeplvlk 15
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                                                            Conservative
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100.0%;
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                                                            0;
                                                                          Score 72;
Pred. No.
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                                                              Mismatches
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                                                                          DB 18;
0.0023;
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Search completed: April 24, 2002, 09:17:37 Job time: 141 sec

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OM protein - protein search, using sw model Run on: April 24, 2002, 09:24:54; Search time 21.46 Seconds (without alignments) 51.256 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score: Sequence:

US-09-689-469-5 30 1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 100059 segs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result

Description Q15109 homo sapien Q62151 mus musculu Q63495 rattus norv Q28173 bos taurus P44688 haemophilus P35949 pneumonia v P53305 saccharomyc Q78477 quillardia P45023 haemophilus P65268 canine aden Q65962 canine aden Q65962 canine aden Q65962 canine aden Q65963 canine aden Q96690 canine aden Q96690 canine aden Q96595 vibrio algi P56346 chlorella v Q9hjtl thermoplasm Q09415 caenorhabdi Q6639 methanobact P41595 homo sapien Q02152 mus musculu Q43278 homo sapien P32966 pseudomonas Q05947 rickettsia Q07170 mycobacteri Q28056 bos taurus Q12797 homo sapien P44408 haemophilus P45998 haemophilus P45999 haemophilus
41 64 10 8 8 6 10 7 8 4 8 2 2 10 8 10 4 10 8 10 7 10 7
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RS9_SULAC	BARW_HORVU	REV_HV1MN	HMGZ_DROME	RS20_CHLPN	VE4_HPV51	MLEV_MOUSE	RRPO_TACV	BAT2_HUMAN	VNUA_PRVKA	KF1C_HUMAN	KF1D_RAT
P39468 sulfolobus			Q06943 dro	Q9z7f2 chlamydia p			P20430 tacaribe vi		P33485 pseudorabie		O35787 rattus norv

# ALIGNMENTS

R R R R R R R R R R R R R R R R R R R	RESULT RAGE_H ID R ACC ACC ACC ACC ACC ACC ACC ACC ACC AC
MEDLINE-SENDAN N.A. (ISOFORM 1). Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Inoko H., Ikemura T.; "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; Genomics 23:408-419(1994).  SEQUENCE FROM N.A. (ISOFORM 1). Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Spies T., Hood L.; Submitted (FEB-197) to the EMBL/GenBank/DDBJ databases.  SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100. Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y., Yamamoto H.; "Molecular heterogeneity of the receptor for advanced glycation endproducts."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  SEQUENCE FROM N.A. (ISOFORM 2). Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; "CNA cloning of a novel secreted isoform of the human Receptor for Advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant sumyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  SEQUENCE OF 1-12 FROM N.A.	LT 1  RAGE_HUMAN STP  OJS109; OJS279; OS  O1-NOV-1997 (Rel.  O1 NOV-1997 (Rel.  20-AUG-2001 (Rel.  ADVANCED GLYCOSYLP  (RECEPTOR FOR ADVP  AGER OR RAGE.  HOMO Sapiens (Huma  EUKARYOTA; BUTCHET  MCBI_TAXID-9606;  [1]  SEQUENCE FROM N.A.  TISSUE-Lung;  MEDLINE-92340547;  Neeper M., Schmidt  Elliston K., Sterr  "Cloning and expre glycosylation end J. Biol. Chem. 267  [2]

B.I.,

Futers T.S.;

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Query Match
Best Local
  Matches
                                                                CONFLICT
SEQUENCE
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VARSPLIC
VARSPLIC
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Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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"Novel
                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECRETED (ISOFORM 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (ARE PRODUCED BY ALTERNATIVE SPLICING TISSUE SPECIFICITY: ENDOTHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                         1; PF00047; 1g; 2.

KT; SM00408; IGc2; 1.

KT; SM00410; IG_like; 1.

SITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; M91211; AAA03574.1; -.
; D28769; BAA05958.1; -.
; U89336; AAB47491.1; -.
; AB036432; BAA89369.1; -.
; AJ133822; CAB43108.1; -.
; AF208289; AAG35728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: ENDOTHELIAL CELLS. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATE IN DIABETES
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  l Similarity
30; Conserv
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1 22
23 404
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Ig_like.
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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POTENTIAL.
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N-LINKED (G
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GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRA
VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAAL
 Score 30; DB
Pred. No. 2.9
); Mismatches
                                                                                                     GACRTESVGGT
Q -> R.
                                                                                                                             LIGVILWQRRQRRGEERKAPENQEEEEERAELNQSEEPEAG
ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
PGPGDPGRPGDSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
                                                                                                                                                                                                                                                                                                                                                ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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             DB 1;
2.9e-25
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AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

Query Match Best Local Similarity

100.0%; 43.3%;

Score 13; Pred. No.

DB 1; I

Length 403

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RAGE_MOUSE
ITD RAGELM
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ACT COLL
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Q62151;
                            CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed: Usage by are entitles requires a licence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E., Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.; "Recombinant advanced glycation end product receptor pharmacokinetics in normal and diabetic rats."; Mol. Pharmacol. 52:54-62(1997).

-i- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMILATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATE WHICH ACCUMILATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATE
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTO
RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                                                                              Immunoglobulin
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
       SEQUENCE
                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003600; Pfam; PF00047; 19; 3
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MEDLINE=97368045; PubMed=9224812;
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Mammalia; Eutheria;
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TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
2 C2-LIKE AND ONE V-LIKE DOMAINS.
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SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                            IG_MHC; 1.
nain; Glycoprotein; Transmembrane; Signal.
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Ig_like.
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Rođentia;
         42668
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       WW;
                                                                     CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                            N-LINKED
                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                   ADVANCED GLYCOSYLATION END PRODUCTSPECIFIC RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
    -LINKED (GLCNAC. . .)
-LINKED (GLCNAC. . .)
1279796FD1579357 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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         CRC64;
                                                                                                                                          21
                            (POTENTIAL).
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         CARBOHYD
SEQUENCE
                                                                       DISULFID
DISULFID
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                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAT
                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L33413; AAA42027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-Lung; MEDLINE-97368045; PubMed-9224812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q63495;
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGER OR RAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAGE_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                          [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ENONTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOSCIOBULIN SUPERFAMILY. CONTAINS
2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROBUCT. ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATE IN DIABETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNITARIGEPLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                               PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C., Chappey O., Wautier M.P., Nagashima M., J., Zhao L., Schmidt A.M., Scherrmann J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                            domain; Glycoprotein; Transmembrane; Signal.

1 22 POTENTIAL.

3 402 ADVANCED GLYCOSYLATION END PRO
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement (See http://www.isb-sib.ch/announce/
           WW;
IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. . . ) (POT

N-LINKED (GLCNAC. . . ) (POT

M; 594481BC3A51E94E CRC64;
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                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                          ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Wautier J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           уд
                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions on
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RESULT
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Best Local :
                 DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410. TO 11.
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Q28173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR
RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91ycosylation end products of proteins.
J. Biol. Chem. 267:14998-15004(1992).
-!- FUNCTION: MEDIATES INTERACTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neeper M., Schmidt A.M., Brett J., Yan S.I
Elliston K., Stern D., Shaw A.;
"Cloning and expression of a cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
    CARBOHYD
                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                      EMBL; M91212; AAA03575.1;
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92340547; PubMed=1378843;
Neeper M., Schmidt A.M., Brett J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGER OR RAGE
                                                                                          DOMAIN
                                                                                                          DOMAIN
                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                               Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QNITARIGEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROT
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHICH ACCUMULATE IN VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNITARIGEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                              PS00290;
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                                                                                                                                                                                                                  domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                           IG_MHC; 1.
nain; Glycoprotein; Transmembrane; Signal
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416
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                                                                                                                                                                                                                                                                                     Ig_MHC.
Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND PARTIAL
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100.0%
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                                           ADVANCED GLYCOSYLATION END SPECIFIC RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
POTENTIAL.
POTENTIAL.
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Pred. No.
POTENTIAL.
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                   GLYCOSYLATION END RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.D.,
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0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                         There are no
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTH_HAEIN
P44688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
the Euro
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                             DNA repai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and influenzae Rd."; Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
DNA MISMATCH REPAIR PROTEIN MUTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAEIN
  VGLF_PVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTH OR HI0403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 CKGAPKKPPQ 47
                                                                                                                                                                          4 ITARIGE
                                                  6
                                                                                                                                                                                                                                                                                                                                                                   repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                             ITARIGE
                                                                                                                                                                                                                                                                                                                                                                                          HI0403;
                                                                                                                                                                                                                                                                                                                                                                                                                U32723; AAC22062.1; P06722; 2AZO.
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10; Conservative
                                                                                                                                                                                                                    7; Conserv
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416 AA;
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223 AA; 24906 MW; 339A4EF9DA0E622A
                                                                                                                                                                                                                         Conservative
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
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                                                                                                                                                                                                                  Score 7; DB 1
Pred. No. 1.3
0; Mismatches
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Pred. No.
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  PRT;
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  537
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0.0013;
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                                                                                                                                                                                                                                                                    Length 223;
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YG4L_YEAST
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01-OCT-1996
15-JUL-1998
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                  YG4L_YEAST
P53305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
CHAIN
CHAIN
Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                 YGR215W.
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                                                                                                                     HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramyxoviridae;
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                                                                                                                                                                                                                                                                                                                                                                   434 GEPLVLK
                                                                                                                                                                                                                                                                                                                                                                                                                9 GEPLVLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
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537
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L 12.4
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P35949;
O1-JUN-1994 (Rel. 29, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSI-
FUSION GLYCOPROTEIN F1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chambers P., Pringle C.R., Easton A.J.;

"Sequence analysis of the gene encoding the fusion glycoprotein of pneumonia virus of filce suggests possible conserved secondary structure elements in paramyxovirus fusion glycoproteins.";

J. Gen. Virol. 73:1717-1724(1992).

-1- FUNCTION: THIS PROTEIN DIRECTS FUSION OF VIRAL AND CELLULAR MEMBRANUS, RESULTING IN VIRAL PENETRATION, & CAN DIRECT FUSION INFECTED CELLS WITH ADJOINING CELLS, RESULTING IN THE FORMATION
                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D11128; BAA01902.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=92333256; PubMed=1629698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; fusion_gly; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GI
                                                                                                                                                                                                                                                                                                                                                                                                 23.3%;
ilarity 100.0%;
Conservative
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,n protein; ?
22
537
101
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514
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463
463
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of mice (PVM)
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                                                                                    34, Created)
34, Last sequence update)
36, Last annotation update)
KDA PROTEIN IN NABIA-GPI1 INTERGENIC
  Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

BA6116EE2FABE702 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
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pneumovirus.
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Saccharomyces
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15-DEC-1998
15-DEC-1998
20-AUG-2001
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                    complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
J. MOI. EVOI. 48:236-244(1999).
-!- FUNCTION: SEEMS TO BE REQUIRED FOR THE ASSEMBLY OF THE PHOTOSYSTEM I COMPLEX (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE-ASSOCIATED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _GUITH
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                                           InterPro; IPR003359; Pfam; PF02392; Ycf4;
                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      SIMILARITY).
-!- SIMILARITY: BELONGS TO THE YCF4 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guillardia theta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRAIN=S288C;
                                                                                         EMBL; AF041468; AAC35658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99128221; PubMed=9929392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          las S.E., Penny S.L.;
plastid genome of the cryptophyte alga,
plastid genome and conserved synteny group
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S0003447; YGR215W.
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  Thylakoid; Transmembrane; Chloroplast 41 POTENTIAL.
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37, Last sequence up
40, Last annotation
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                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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YA79_HAEIN
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01-OCT-1996
01-NOV-1997
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                                                                                                                          Pfam; PFC PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT
SYSTEM FOR AN AMINO-ACID. PROBABLY RESPONSIBLE FOR THE
TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=RD / KW20 /
                                                 TRANSMEM
                                                                                                  Hypothetical protein;
                                                                                                                                                                                                   EMBL; U32788; AAC22735.1; TIGR; HI1079; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
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MEDLINE=95350630; PubMed=7542800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMO
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PS00402; BPD_TRANSP_INN_MEMBR;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat)
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SEQUENCE
                                                                                                   E434_ADECT STANDARD; PRT; 259 AA. P87568; 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EARLY E4 30 KDA PROTEIN.
Canine adenovirus type 2 (strain Toronto A 26-61).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baer R., Bankier A.T., Biggin M.D., De Glbson T.J., Hatfull G., Hudson G.S., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B9 Nature 310:207-211(1984).
SEQUENCE FROM N.A. Campbell J.B., Zhao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V01555; CAA24835.1; -. PIR; A03787; QQBE43. PIR; S33040; S33040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaherpesvirinae; Lymphocryptovirus, NCBI_TaxID=10377;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
01-DEC-192 (Rel. 24, Last annotation
PROBABLE MEMBRANE ANTIGEN GP85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEBV
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184 LVLKCK
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665962;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenovirus type 2.";
Submitted (NOV-1996) to
-!- SIMILARITY: BELONGS
FAMILY.
                                                                                                                                                                                                                                                                                                                        Dragulev B.P., Sira S., Abouhaidar M.G., Cam "Sequence analysis of putative E3 and fiber strains of canine adenovirus type 1."; Virology 183:298-305(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine adenovirus type 1 (strain CLL) Viruses; dsDNA viruses, no RNA stage; NCBI_TaxID=69150;
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                                                                                  Early protein
SEQUENCE 26
                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 248-265 FROM N.A. MEDLINE=91272490; PubMed=1828920;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Campbell J.B., Zhao Y.; Submitted (AUG-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 31 KDA PROTEIN.
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SEQUENCE 25
                                                                                                                    EMBL; U55001; AAB05452.1;
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                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
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Canine adenovirus type 1 (strain RIZ61).
Canine adenovirus type no RNA stage; Adenoviridae; Mastadenovirus
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MOTRISON M.D., ONIONS D.E., NICOLSON L.;
"Complete DNA sequence of canine adenovirus
J. Gen. Virol. 78:873-878(1997).
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                                                 European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                              Nakamura T., Katoh Y., Shimizu Y., Matsuba Y., Unemoto T.; "Cloning and sequencing of novel genes from Vibrio alginolyticus support the growth of K+ uptake-deficient mutant of Escherichia coli.";
                                                                                                        PROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP SEQUENCE 278 AA; 29815 MW; 50359E5EF970
                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1277:201-208(1996).
i- CATALTTIC ACTIVITY: L-PROLINE + NAD(P).
CARBOXYLATE + NAD(P)H.
-i- PATHWAY: TERMINAL (THIRD) STEP IN PROL
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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InterPro; IPRUUJU.
Pfam; PF00047; 1g; 3.
SMART; SM00410; IG_11ke; 1.
SMART; SM00410; IG_MC; UNKNOWN_1.
SMART; SM00410; IG_MC; UDKNOWN_1.
TROSITE; P500290; IG_MC; UDBFDC50A6C8CB902 CRC64;
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01-JAN-1998
01-JUN-2001
                                                                                                                                                                                            Schmidt A.M., Vianna M., Gerlach M., Brett J., Ryan J., Kao J., Esposito C., Hegarty H., Hurley W., Clauss M.;
"Isolation and characterization of two binding proteins for advanced glycosylation end products from bovine lung which are present on the endothelial cell surface.";
J. Biol. Chem. 267:14987-14997(1992).
SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;
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Schmidt A.M., Vianna M., Gerlach M.,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Loretz C., Schmidt S., T
Submitted (OCT-1997) to
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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROWER L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S., Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                     Chem. 20, E 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                  Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig_c2.
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Ig_MHC.
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Last sequence up
                                  0;
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Pred. No.
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                                  Mismatches
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                                                           . DB
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on update)
                                                                                          Length 32;
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                                  Indels
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RA Adams N.D., Celniker S.E., Hilt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hilt R.A., Evans C.A., Golayne J.D.,
RA George R.A., Lewis S.E., Richards S., Asiburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asiburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Burtis K.C., Bater E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Davies M., J., J., Lai Z.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Linko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Ketchum K.A.,
RA Harris M., Walley D., Mcherson D.,
RA Ra Levits P., Sand J., Walley D., Malley D., Malley D.,
RA Ra Levits P., San
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01-MAY-2000
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                                                                                                                                           FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
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                                                                                                                                                                                         AE003828; AAF58764.1;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, ) (TrEMBLrel. 13, ) (TrEMBLrel. 13,
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23.3%;
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Last sequence update)
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   Score 7;
Pred. No.
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                                                                                                                                C050101AD183FAF7 CRC64;
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                                 Length 237;
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Best Local S
Matches 7
STRAIN-Z2491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE-20222556; PubMed-10761919;

Parkhill J., Achtman M., James K.D., Bent

Klee S.R., Morelli G., Basham D., Brown D

Davies R.M., Davis P., Devlin K., Feltwel

Jagels K., Leather S., Moule S., Mungall
                                                                                                                                                                                                                          Q9JX44
Q9JX44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MC58 / SEROGROUP B;
MEDLINE-2017575; PUBMed-10710307;
MEDLINE-2017575; PUBMed-10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Reison W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Lickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B Hason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E. Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9K1F6;
                                                                                                                                                                  01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00849; PseudoU_synth_2; 1
Pfam; PF01479; S4; 1.
ProDom; PD001819; PseudoU_synth;
SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MC58 / SEROGROUP
MEDLINE=20175755; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup Bacteria; Proteobacteria; beta sul NCBI_TaxID=491;
                                                                                                                            Neisseria meningitidis (se Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Neisseria MC58.";
                                                                                     SEQUENCE FROM N.
                                                                                                               NCBI_TaxID=65699;
                                                                                                                                                        RIBOSOMAL LARGE
RLUC OR NMA0070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE002377; AAF40655.1; TIGR; NMB0198; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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IPR002990; PSI_RLU.
IPR002942; S4.
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nilarity 100.0%;
Conservative 0
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                         (serogroup
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15, Last sequence update)
17, Last annotation update)
PSEUDOURIDINE SYNTHASE C.
                                                                                                                            beta
                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 2; Pred. No. 12; 0; Mismatches
                                                                                                                                                                                                                                         PRT;
 K.D., Bentley S.D., Churche D., Brown D., Chillingworth K., Feltwell T., Hamlin N., Mungall K., Quail M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oup B).
subdivision;
                                                                                                                           sup A).
subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                       F2058C52ACE443EC CRC64;
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                                          Churcher
                                                                                                                                                                     4.2.1.70).
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                 Holroyd
                                                                                                                            Neisseria
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RESULT
Q9LQP6
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Best Local
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EMBL; AL162752; CAB83386.1; .

InterPro; IPR000613; PseudoU_synt
InterPro; IPR002990; PSI_RLU.

InterPro; IPR002942; $4.

Pfam; PF00849; PseudoU_synth_2; 1
Pfam; PF01479; $4; 1.
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01-0CT-2000
01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                   EMBL; AC007583; SEQUENCE 595 i
                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F24B9.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01479; S4; 1. ProDom; PD001819; PseudoU_synth;
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                                                                                                                                              Submitted
                                                                                                                                                                        Theologis;
                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                       Theologis
                                                                                                                                                                                                                                                                                                          STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 GEPLVLK
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                                                                                              (JUN-2000) to the 07583; AAF75084.1; 595 AA; 63982 My
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O (TrEMBLrel.
O (TrEMBLrel.
                                                                                                                                                                                                                                                                                                          COLUMBIA;
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100.0%;
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PSI_RLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                   FF5B15F9BB28B87E
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9 7;
No.
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Query Match Best Local Similarity

23.3%;
100.0%;

Score Pred.

DB 20;

10;

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holtards S.A., Sabhurner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burkova D., Botchan M.R., Bouck J., Bhandari D., Bolshakov S.,
RA Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borlova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Keland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Melnst B., McIntosh T.C., McLedd M.P., McPherson D.,
RA McIntosh T.C., Schepter F., Shen H.,
RA McIntosh J., Keltosh F., Karpen G.H., Ke Z., Liang Y., Lin X.,
RA McIntosh J., Keltosh F., Karpen G.H., Ke Z., Liang
       Matches
                     Query Match
Best Local :
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Q9W322;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Diracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-JUN-2001
                                                                             Pfam; PF02712;
SEQUENCE 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                         InterPro;
                                                                                                                      FlyBase; FBgn0030148; CG3106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
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    Similarity 7; Conserv
                                                                                                         IPR003862;
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      Conservative
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23.3%; 5c.
100.0%; Pr
                                                                                                         UPF0063
                                                                             MW;
    Score 7; DB 5; Pred. No. 24; 0; Mismatches
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Last sequence update)
Last annotation update)
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            DB .
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    0;
                               Length 742;
                                                                             CRC64;
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Q9NFJ5
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Best Local :
Matches
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SEQUENCE
Q9N6I0 PRELIMINARY; PRT;
Q9N6I0;
01-OCT-2000 (TrEMBLrel. 15, Created)
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Thesis (2000), Department
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID-5702;
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Eukaryota; Euglenozoa; Ki
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NCE 61 AA;
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01-JUN-2001 (TrE
HISTONE H1.
H1E76 OR H1F76.
Q9FR57;
Q9FR57;
01-MAR-2001
01-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cystein proteinase inhibitor.";
Submitted (MAY-1998) to the EMBI
EMBL; AB014760; BAA28867.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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EMBL; AJ287601; CAB76186.1; -.
EMBL; AJ287601; CAB76186.1; -.
INTERIPRO 13186; Linker_histone.
PRINTS; PRO0624; HISTONEH5.
SEQUENCE 76 AA; 7573 MW; 6079EF4
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
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NCBI_TaxID=5702;
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InterPro; IPR003243; Cystatin_C_M.
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eudicots; Rosid
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PRUGLI L., Lifschitz E.;
Submitted (AUG-1999) to th
EMBL; AF175963; AAG43410.1
SEQUENCE 99 AA; 11408 M
                Q9EAJ5;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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neoplasia.";
Clin. Diagn. Lab. Immunol. 7:91-95(2000)
Clin. Biagn. Lab. Immunol. 7:91-95(2000)
Chin. Biagn. Lab. Immunol. 7:91-95(2000)
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Submitted
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MEDLINE-20087389; PubMed-10618284;

Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;

"Molecular cloning and nucleotide sequence analysis of a novel h
papillomavirus (type 82) associated with vaginal intraepithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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NON_TER 1 1 11
SEQUENCE 101 AA; 112
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OS Human immunodeficiency virus type 1
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxLD=11676;
RN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIM=99-117635;
RR Barlow K.L., Tatt I.D., Cane P.A., Pillay D., Clewley J.P.;
RT "Detection of simple and complex recombinant strains of HIV-1 in the RT UK."; Tatt PROFESSE BELONGS TO PEPTIDASE FAMILY A2; ALSO CLEWLEY, THE PROFESSE BELONGS TO PEPTIDASE FAMILY A2; ALSO CROSS TO PEPTIDASE FAMILY.

PAGITE: PET TO PETIDASE FAMILY A2; ALSO CROSS TO PEPTIDASE FAMILY.

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PET TO PETIDASE FAMILY A2; ALSO CROSS TO PEPTIDASE FAMILY.

PET TO PETIDASE FAMILY A2; ALSO CROSS TO PEPTIDASE FAMILY.

PET TO PETIDASE FAMILY A2; ALSO CROSS TO PEPTIDASE FAMILY.
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Copyright GenCore version (c) 1993 - 2000 4.5 Compugen Ltd

OM protein - protein search, using sw model

April 24, 2002, 09:19:01; Search time 38.71 Seconds

(without alignments)
59.035 Million cell updates/sec

US-09-689-469-5

Title:

Sequence: Perfect score:

AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0

219241 segs,

76174552 residues

Total number of hits satisfying chosen parameters:

Maximum Minimum DB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pir1:\*
pir2:\*
pir3:\*

score and is No. is the number of results predicted by chance to have greater than or equal to the score of the result being pus derived by analysis of the total score distribution. printed,

#### SUMMARIES

25 27 28 29	19 20 21 23 24	15 16 17	1 2 3 3 4 4 4 6 6 7 7 7 110 111 112 113	Result
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00000	30.99	31.5	100 92.0 89.5 89.5 33.3 33.0 32.7 32.7 32.7 32.7	% Query Match
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transcription fact	transcription fact	probable thra prot	probable transcrip	neurotrophic recep	tyrosine kinase C	neurotrophin-3 rec	neurotrophin-3 rec	DnaJ homolog, 4706	protein UNC-89 - C	neuroglian - fruit	ErbB kinase activa	tapasin 1 homolog,	mutator mutH - Hae	Ig heavy chain V r	platelet-derived g

#### ALIGNMENTS

advanced glycosylation end-products receptor precursor - human N;Alternate names: advanced glycosylation end product-binding | C;Species: Homo sapiens (man) end product-binding protein, 35K; glycoprot

C:Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999
C:Accession: I61596; B42879; S27968

R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.;

Genomics 23, 408-419, 1994
A;Title: Three genes in the human MHC class
nterpart of mouse mammary tumor gene int-3.
A;Reference number: A55562; MUID:95137587
A;Accession: I61596 III region near the junction with the cla

A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A;Molecule type: DNA A;Residues: 1-404 <RES>

A;Cross-references: GB:D28769; NID:g561657; PIDN:BAA05958.1; PID:g561659
R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A;Reference number: A42879; MUID:92340547
A;Accession: B42879

A; Experimental source: lung

A;Molecule type: mRNA A;Residues: 'G',2-99','R',101-404 <NEE> A;Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846

A;Note: sequence extracted from NCBI backbone (NCBIP:109438) C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycellular function, thus contributing to tissue lesions in diabetes. C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

A;Gene: C; Genetics: GDB: AGER

A;Cross-references: GDB:306354; OMIM:600214
A;Map position: 6p21.3-6p21.3
A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2 C; Function

A.Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT F;23-344/Domain: extracellular #status predicted <EXT>
F;33-344/Domain: immunoglobulin homology <IM1>
F;31-210/Domain: immunoglobulin homology <IM2>
F;352-303/Domain: immunoglobulin homology <IM3>

F;345-362/Domain: F;363-404/Domain:

345-362/Domain: transmembrane #status predicted <TMM>
346-362/Domain: intracellular #status predicted <ITMP>
25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted
38-99,144-208,259-301/Disulfide bonds: #status predicted

```
N;Alternate names: advanced glycosylation enu province year and sequence crevision 07-Feb-1997 #text_change 16-Jul-1999
C;Betes: Bos primigenius taurus (cattle)
C;Bete: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: A42879; A42878; S27949
R;Neeper, M; Schmidt, A.M.; Brett, J; Yan, S.D.; Wang, F; Pan, Y.C.; Elliston, K.; St J, Biol. Chem. 267, 14998-15004, 1992
A;Pitle: Cloning and expression of a cell surface receptor for advanced glycosylation en A;Reference number: A42879; MUID:92340547
A;Recession: A42879
A;Molecule type: mRNA
A;Residues: 1-416 <ARE>
A;Accession: A42879; MUID:92340547
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of this sequence, including the amino end of the mature protein, were detered; parts of the mature protein, parts 
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A; Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; A; Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; C; Superfamily: advanced glycosylation end products C; Keywords: receptor; transmembrane protein F; 31-100/Domain: immunoglobulin homology < TMM>
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C;Accession: T09062
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Lusubmitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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A; Residues: 1-402 < ROW>
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N; Alternate names: RAGE
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30; Conservative
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93.1%;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 162; DB 1;
Pred. No. 1.5e-15;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272/3; 320/1; 329/1; 371/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lasky, S.; Loretz, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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F;355-372/Domain: transmembrane #status predicted <TMM>F;373-416/Domain: intracellular #status predicted <INT>F;25,80/Binding site: carbohydrate (Asn) (covalent) #status F;38-98,143-207,269-311/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;23-354/Domain: extracellular #status predicted F;31-100/Domain: immunoglobulin homology <IM1> F;136-209/Domain: immunoglobulin homology <IM2> F;262-313/Domain: immunoglobulin homology <IM3> F;262-313/Domain: transmembrane #status predicted F;373-416/Domain: intracellular #status predicted F;37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-22/Domain: signal sequence #status predicted <SIG>F;23-416/Product: advanced glycosylation end-products predicted <EXT>F;23-354/Domain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: advanced glycosylation end products receptor; C;Keywords: Alzheimer's disease; glycoprotein; receptor; tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ates in the neurotoxic pathway that produces dementia in Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: neuronal receptor for amphoterin, a DNA-binding
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Function:
24
                                                                                                                  N
                                                     QNITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                               89.5%;
89.7%;
                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                               Score 145; DB 1; Pred. No. 4.3e-13;
                                                                                                                                                                                                                                                  Mismatches
52
                                                                                                                                                                                                                                                                                                                                                                     Length 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor RAGE #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein involved
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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hypothetical protein ZC101.2e - Ca C;Species: Caenorhabditis elegans Caenorhabditis elegans

B47648;

submitted to the EMBL Data A; Reference number: Z19182 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 01-Dec-2000 C;Accession: T19821; T19819; T19820; T27489; T27488; T27489; T27487; A47648; A; Molecule type: R; Baynes, A;Cross-references: A;Residues: A; Status: preliminary; translated A; Accession: A; Reference number: 1-3375 <WIL> T19821 DNA Library, from GB/EMBL/DDBJ March

A; Experimental source: clone EMBL: Z93375; PIDN: CAB07569.1; GSPDB: GN00020; ce: clone C38C6 CESP: ZC101

A; Molecule type: DNA A; Status: preliminary; translated from GB/EMBL/DDBJ A; Accession: T19819

A:Residues: 1-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQNGPLSRKTRTTTKLF A;Cross-references: EMBL:Z93375; PIDN:CAB07567.1; GSPDB:GN00020; CESP:ZC101.2a A:Experimental source: clone C38C6 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Accession: T19820

A; Molecule type: DNA
A; Residues: 1-1694,'H',1883-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQN
A; Cross-references: EMBL: Z93375; PIDN: CAB07568.1; GSPDB: GN00020; CESP: ZC101.2c R;Percy, A; Experimental source: clone C38C6

submitted to the EMBL Data Library, March 1997 A; Reference number: Z20375 A; Status: preliminary; translated A; Accession: T27490 from GB/EMBL/DDBJ

A; Molecule type: DNA
A; Residues: 1-3375 <WI2>
A; Cross-references: EMBL: 293395; PIDN:CAB07708.1;
A; Cross-references: clone ZC101 GSPDB:GN00020;

A; Status: preliminary; translated from GB/EMBL/DDB A; Accession: T27488

A; Accession: T27489

A; Molecule type: DNA
A; Residues: 1-1694,'H',1883-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQN
A; Cross-references: EMBL: E93395; PIDN: CABO7707.1; GSPDB: GN00020; CESP: EC101.2c

Status: preliminary; translated from GB/EMBL/DDBJ

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A; Map position: 2

A; Introns: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/
A; Introns: 32/1; 134/1; 225/1; 3813/3; 2863/1; 2900/3; 3084/1; 3176/1; 3250/2

C; Superfamily: LDL receptor ligand-binding repeat homology; laminin-type EGF-like homol C; Keywords: extracellular matrix

F; 149-183/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F; 190-224/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F; 233-268/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F; 355-1002/Domain: Laminin-type EGF-like homology <LDC3>
F; 955-1002/Domain: laminin-type EGF-like homology <LDC3>
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: Z17975 A; Accession: T14316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-546',P',548-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545
A;Cross-references: GB:L13458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-546, 'p',548-2198, 'D',2290, 'NAR',2294, 'L',2296, 'WHATE',2302-2303, 'V',2305,
1, 'ANIV',2516-2517, 'LQQG',2522, 'IDG',2526, 'S',2528, 'SRGFHV',2535, 'F' <RO2>
A;Cross-references: GB:L13458
A;Accession: C47648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: clone ZC101
R;Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
Genes Dev. 7, 1471-1484, 1993
A;Title: Products of the unc-52 gene in Caenorhabditis elegan
A;Reference number: A47648; MUID:93339574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1128,1290, 'DFARNSPS',1299, 'NSS',1303-1304, 'R', 'RHR',1544-1545, 'RIRVRS',15
A; Cross-references: EMBL: E93395; PIDN: CAB07704.1; GSPDB: GN00020; CESP: ZCI01.2b
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A;Accession: T27487
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                             A; Residues: 1-1344
A; Cross-references:
                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1344 < YUA>
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A; Residues: 1-546,'P_,548-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRRNAQNGPLSI
                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: ZC101.2e; CESP: ZC101.2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A47648
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Best Local (
                                                                                             Matches
                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1990 VGEPLQVKCEAFGAPGDPEPEVEW 2013
152
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
                                            3 NITARIGEPLVLKCKGAPKKPPORLEWK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGEPLVLKCK--GAPKKPPQRLEW 29
NVVVAVGEPAVMECVPPKGHPEPLVTWK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                             Conservative
                                                                                                                                                                                                             EMBL: AF060570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%;
                                                                                                              33.3%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB Pred. No. 1.5; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                   Score 54;
Pred. No.
                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                           NID: 94206385; PID: 94206386; PIDN: AAD11628
                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CESP: ZC101.2c;
                                                                                                                                                                                                                                                                               GB/EMBL/DDBJ
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1.5;
                                                                                                                                         DB
                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6,
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                                                                                                                                    Length 1344;
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                                                                                          Indels
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                                                                                     Gaps
                                                                                        0;
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C;Date: 31-Mar-1976, PS0270
C;Accession: JH0506; PS0270
R;Tanaka, H.; Matsui, T.; Agata, A.; Tomur
R;Tanaka, H.; Matsui, T.; Agata, A.; Tomur
Neuron 7, 535-545, 1991
A;Title: Molecular cloning and expression
A;Title: Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Geneti
A; Note:
                                                                                                   adhesion molecule SC1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                                                                                                                                                                RESULT
JH0506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: This is a cell surface glycoprotein.
C;Comment: This protein is localizes to axons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Burns, F.R.; von Kannen, S.; Guy, L.; Ra

Reuron 7, 209-220, 1991

A;Title: DM-GRASP, a novel immunoglobulin

A;Reference number: JH0464; MUID:91337449

A;Accession: JH0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-483 <DUE>
A; Cross-references: EMBL: AL117666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein Sequence A; Reference number: Z18727 A; Accession: T17346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp58601624.1 - C:Species: Homo sapiens (man) C:Date: 15-Oct-1999 #sequence_revision
A; Reference number: JH0506; A; Accession: JH0506
                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-32/Domain: signal sequence #status predicted < F;33-587/Product: DM-GRASP #status predicted <DMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1992 #sequence_revision
                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-587 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DM-GRASP precursor - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T17346
                                                                                                                                                                                                                                                                                                                                                                                                      F;67,198,270,311,365,461,484,503/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: JH0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: adult
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Local Similarity 40.0%;
nes 10; Conservative
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10; Conserv
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Pred. No. 9.
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Pred. No. 6.
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Ryfalls, D.L.; Rosen, K.m.; Corrections of the Stimulates of A.Title: ARIA, a protein that stimulates of the Stimulates 
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A; Residues: 34-48 <TAN1>
A; Residues: 34-48 <TAN1>
C; Comment: This protein is uniquely and transiently expressed on C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
F; 1-33/Domain: signal sequence #status predicted <SIG>
F; 34-588/Product: adhesion molecule SCI #status predicted <ADH>
F; 500-523/Domain: transmembrane #status predicted <TRAN
F; 101,173,199,271,312,366,462,485,504/Binding site: carbohydrate
                                                                                                                                      A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIN:127787, C; Superfamily: unassigned EGF-related proteins; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetylcholine receptor synthesis stimulator ARIA-1 C;SpecLes: Gallus gallus (Chicken) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: A45769
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A45769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M. Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
A;Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is A;Reference number: A45254; MUID:92302224
A;Accession: A45254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface glycoprotein BEN precursor - chicken
C;Specles: Gallus gallus (chicken)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
C;Accession: A45254; S19202
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A; Molecule type: mRNA
A; Residues: 1-588 <POU>
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A; Cross-references: GB:563276
A; Experimental source: embryo
A; Accession: pS0270
                                                                                                                                                                                                                    A;Cross-references: GB:L11264; NID:g212603; PIDN:AAA49037.1; PID:g212604
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A; Residues: 1-602 <FAL>
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Pred. No.
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  7;
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7; Mismatches
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elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision
C;Accession: I38346
R;Labeit, S.; Kolmerer, B.
                                                                                                                                         RESULT
I38346
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A;Description: appears to C;Keywords: transmembrane
                                                                                                                                                                                                                                                                                      R;Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, Cell 92, 205-215, 1998
A;Title: Roundabout controls axon crossing of the CNS midline and defines a novel A;Reference number: Z17897; MUID:98117249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The mouse he
A; Reference number: Z20879
A; Accession: T30805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, I submitted to the EMBL Data Library, July 1998 A;Description: The mouse homologue of human DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: transmembrane receptor protein Robol homolog
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1651 <KID>
                                                                                                                                                                                                                                A;Status: preliminary; translated A;Molecule type: mRNA
                                                                                                                                                                                                                                                                        A; Accession: T14160
                                                                                                                                                                                                                                                                                                                                                                                     C; Date: 20-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1612 <WUM>
                                                                                                                                                                                            A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane receptor protein Robol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 DVMVAVGEPAVMECQPPRGHPEPTISWK
                                        Local Similarity
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3 NITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NITARIGEPLVLKCKGAPKKPPQRLEWK 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     T14160
                                          Conservative
                                                                                                                                                                                          EMBL: AF041082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL:Y17793; NID:e1329712; PID:e1329713; PIDN:CAA76850.1
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                                                                                                                                  function protein
                                                        32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%;
                                  7;
                                                        Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
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                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                      as
                                                                                                                                                                                            NID: g2811215; PID: g2811216; PIDN: AAC39960.1
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                    the gatekeeper
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27;
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                                                                          Length 1651
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                                      0;
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                                      0;
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29-May-1998 #text\_change 21-Jul-2000

A;Reference number: A57430; MUID:96026330
A;Accession: I38346
A;Status: preliminary; translated from GB/EMBL/DDBJ

Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330

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R; vermeer, H.; Warmerdam, G.W.; de Boer, H.A.; Verbeet, M.P.H. submitted to the EMBL Data Library, September 1994
A; Description: The cloning, tissue specific expression and interspecies sequence compari A; Reference number: $48841
A; Statuto, 198841
A; Statuto, 198841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Didicus, Procession A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-757 < VER>
A; Residues: 1-757 < VER>
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; NID: g563340; PIDN: CAA57136.1; PID: g563341
A; Cross references: EMBL: X81371; PID: g563340; PID: g563341
A; Cross references: EMBL: X81371; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;631-633/Domain: transmembrane #status predicted <TMM>
F;654-757/Domain: intracellular #status predicted <INT>
F;654-757/Domain: intracellular #status predicted <INT>
F;40-110,56-64,152-220,166-173,257-324,271-279,370-440,384-394,481-543,495-502/Disulfide F;83,420,468/Binding site: carbohydrate (Asn) (covalent) #status predicted F;665/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;19-572/Product: free secretory component #status F;33-112/Domain: immunoglobulin homology <IM1> F;145-222/Domain: immunoglobulin homology <IM2> F;250-328/Domain: immunoglobulin homology <IM2> F;250-328/Domain: immunoglobulin homology <IM3>
                                             polymeric immunoglobulin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997
C;Accession: I45956
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C;Keywords: duplication; glycoprotein; immunoglobulin receptor; phosphoprotein; transcyt
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-757/Product: transmembrane secretory component #status predicted <MATM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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I45956
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A; Residues: 1-7962 < RES>
R; Kulseth, M.A.; Krajci, P.; Myklebost, O.; Rogne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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nes 11; Conserv
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Pred. No.
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24;
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A; Molecule type: mRNA
A; Residues: 1-757 <KUIL>
A; Cross-references: GB:L04797; NID:g388279; PIDN:AAC41620.1; PID:g388280
C; Superfamily: secretory component; immunoglobulin homology
F;145-222/Domain: immunoglobulin homology <IMM>
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 В
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                                                                                                                                                                                                                                                                  A; Reference number: I45956; MUID:95186063
A; Accession: I45956
                                                                                                                                                                                                                                                                                                     A; Title: Cloning and characterization of two forms of bovine polymeric immunoglobulin
                                                                                                                                                                                                                                                                                                                        DNA Cell Biol. 14, 251-256, 1995
                                                                                      Query Match
Best Local
                                                                      Matches
 467
                                 2 QNITARIGEPLVLKC 16
 KNVTAWLGEPLKLSC
                                                                    Similarity 9; Conserv
                                                                    Conservative
                                                                                      31.5%;
481
                                                                      ω
••
                                                                                    Score 51;
Pred. No.
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                                                                      Mismatches
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24;
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                                                                      Indels
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Search completed: April 24, Job time: 202 sec

2002,

09:19:03

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
           Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
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length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-633-148-13
US-08-633-148-5
US-08-633-148-5
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US-08-434-678-2
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US-08-684-3839-2
US-08-68-332-538-15
US-08-814-15-16-8
US-08-814-15-16-8
US-08-8174-678-2
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Sequence 12, Appli
Sequence 13, Appli
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48.5	48.5	49	49	49	49	49	49	49	49	49	49	49	49	50	50	50	51
29.9	29.9	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.9	30.9	30.9	31.5
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US-08-469-537A-105	US-08-795-868-16	US-09-398-496-32	US-08-753-007A-32	US-08-752-307B-9	US-09-398-496-8	US-08-753-007A-8	US-08-660-531-5	US-08-659-984A-5	US-08-660-531-1	US-08-659-984A-1	US-09-398-496-6	US-08-753-007A-6	US-08-429-742-4	US-08-752-307B-10	US-08-427-497E-22	US-08-341-843B-17	US-09-098-707A-2
ζ,	Sequence 16, Appl	Sequence 32, Appl		9,		Sequence 8, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 22, Appl	Sequence 17, Appl	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-08-633-148-4

Sequence 4, Applic Patent No. 5864018

Application

US/08633148

GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL

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                                                          Query Match
Best Local S
Matches 30
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FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 'Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                    LENGTH:
1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
                                                          1 Similarity 30; Conserv
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                                                          0;
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                                                        Score 162; DB 2;
Pred. No. 2.1e-15;
); Mismatches 0;
                                                                                            Length 318;
                                                          Indels
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AQNITARIGEPLYLKCKGAPKKPPQRLEWK 30

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US-08-633-148-2
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Best Local (
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                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: U5.708/633,148 FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDITOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                     CORRESPONDENCE ADDRESS:
                                                                                        NUMBER OF SEQUENCES:
                                                                                                       TITLE OF INVENTION: CD6 LIGAND
                                                                                                                                                                               APPLICANT:
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                                                                                                                          APPLICANT:
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                                                                                                                                                            PPLICANT:
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                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                  ADDRESSEE:
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CALIFORNIA
               SEE: NIXON & VANDERHYE P.C.: 1100 NORTH GLEBE ROAD ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
VIRGINIA
                                                                                                                                       ARUFFO, ALEJANDRO PATEL, DHAVALKUMAR BOWEN, MICHAEL A.
                                                                                                                          MARQUARDT, HANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                  HAYNES, BARTON F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
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100.0%; ; 1
htive 0;
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Pred. No. 2.3e-15;
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US-08-684-594-5
                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                TELEFAX: (703) 816-410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                               Local Similarity 100.0%; nes 23; Conservative (
                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: WILSON, MARY J. REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 01
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                               8 IGEPLVLKCKGAPKKPPQRLEWK 30
                                                                                                                                                                                                                                                                                    amino acid
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DR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                  79.68;
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                                                                                                                                                                                                                                                                                                                                                                                                      1579-95
                                                                                                                                               Score 129; DB 2; Pred. No. 8.5e-1
                                                                                                                                 0;
                                                                                                                                 Mismatches
                                                                                                                                                             Length 278;
                                                                                                                                 Indels
                                                                                                                                 0,:
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Sequence 5 Patent No. GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: STREET: 1100 CITY: ARLINGTON STATE: VIRGINIA STATE: U.S.A. APPLICANT: APPLICANT: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CORRESPONDENCE ADDRESS: APPLICANT: MARQUARDITITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT: APPLICANT: APPLICATION NUMBER: FILING DATE: 18-JU ADDRESSEE: 22201-4714 Application US/08684594 E: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD MARQUARDT, HANS VENTION: CD6 LIGAND ARUFFO, ALEJANDRO HAYNES, BARTON F. BOWEN, MICHAEL A. PATEL, DHAVALKUMAR 18-JUL-1996 US/08/684,594 US 08/432,016

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

01-MAY-1995

APPLICATION NUMBER: US 0: FILING DATE: 02-NOV-1994

US 08/333,350

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-633-148-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Applic
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Best Local Similarity
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                                                                       TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
             SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                              APPLICATION NUMBER: US/08/633,148 FILING DATE: 16-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
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STRANDEDNESS:
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100.0%; Pre
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Pred. No.
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RESULT 7
US-08-633-148-5
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Sequence 5, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08633148 Patent No. 5864018
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              LD NO:
LACACTERISTICS:
LA: 15 amino acids
LYPE: amino acid
STRANDEDNESS: $4
TOPOLOGY: 1'
(OLECULE ''
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NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 0146
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
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                                                                                                                                                                1 AQNITARIGEPLVLK 15
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16-APR-1996
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100.0%;
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ER: 014618-005600US
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Pred. No.
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ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: U5.08/633,148 FILING DATE: 16-APR-1996
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NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 0146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
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CURRENT APPLICATION DATA:
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ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
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APPLICANT: HOLLANDER, DORIS A.
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                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                             94111
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5864018
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PENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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100.0%; Pred. No.
tive 0; Mismatc
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US-08-168-091A-2
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; MOLECULE TYPE: protein US-08-168-091A-2
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Patent No.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                      CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,742

FILING DATE: 29-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fischbach, Gerald.
APPLICANT: Falls, Douglas R.
APPLICANT: Rosen, Kenneth M.
APPLICANT: Corfas, Gabriel
TITLE OF INVENTION: Neurotroph
NUMBER OF SEQUENCES: 47
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                                                                                              TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
                                                                                                                            REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
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NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: C. Boston
                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 CKGAPKKPPQ 25
                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 15-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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3. 5665862
                                                                                                                                                                                                                                                                                                                                                                                                                        02109
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                                            amino acid
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60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                  linear
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                                                                                                                                                                                                                                                                                         15-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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Pred. No.
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0.012;
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Query Match

33.3%;

Score 54;

DB 1;

Length 602;

Wed Apr 24 09:48:10 2002

MARQUARDT, HANS

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; Sequence 2, Application US/08986485
; Patent No. 6046030
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                                                                                                        US-08-432-016-3
                                                                                                                          RESULT
                                                         Sequence 3, Application US/08432016 Patent No. 5968768 GENERAL INFORMATION:
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 32.1%; Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 60/059,448
APPLICATION NUMBER: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
                            APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
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APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
                                                                                                                                                                     714 VGETVALQCK-ATGNPPPRITW 734
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CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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:| :|: |||:|: : | | :|
                                                                                                                                                                                             IGEPLVLKCKGAPKKPPQRLEW
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ARUFFO, ALEJANDRO
PATEL, DHAVALKUMAR
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                                                                                                                                                                                                                                                                                                                           protein
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45.5%;
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Pred. No. 1
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; MOLECULE TYPE: protein US-08-432-016-3
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                                                                                                                                                                                                                                                                                                              Sequence 3, Applic Patent No. 5998172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/432,016
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 3:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                           APPLICANT: MARQUARDT, HANS TITLE OF INVENTION: CD6 LIGAND
                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                           APPLICANT:
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                        STREET: 1100 NOI CITY: ARLINGTON STATE: VIRGINIA
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                                                        COUNTRY: U.S.A. ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AQNITARIGEPLYLKCKGAPKKPPQ 25
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WILSON, MARY J.
"YON NUMBER: 32,955
"YON NUMBER: 1579-95
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                                                                                                                                                                                                                                         HAYNES, BARTON F.
ARUFFO, ALEJANDRO
PATEL, DHAVALKUMAR
                                                                                                                                                                                                                             BOWEN, MICHAEL A.
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Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/432,016
APPLICATIO
                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FILING DATE: 25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/143,903 FILING DATE: 02-NOV-1993 ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 SQSSTIKEGDNVTLKCSGNGNPPPQ 245
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
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Local Similarity 40.0%;
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                                 NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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REFERENCE/DOCKET NUMBER: 853D4
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California
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WILSON, MARY J.
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n Release #1.0, Version #1.30
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5; Mismatche
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QNITARIGEPLVLKCKGAPKKPPQRLEW 29

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DO SOFTWARE: patin (Genen CURRENT APPLICATION DATA:
                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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MEDIUM TYPE: 5.25 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: Genentech; Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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TELEFAX: 415/952-98
TELEX: 910/371-7168
               Local
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TELEX: 910/371-7168
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                                                                                                                                                                                                                                                                                                                           FILING DATE: 25 CLASSIFICATION:
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 Similarity 9; Conser
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             32.7%;
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Score 53; DB Pred. No. 11; 7; Mismatches
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RESULT 15

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Sequence 5,756121

EMERA IN MORMATION:

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CHAPTESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS

CONTROL ON NEURONS:

TO AXONIN ON NEURONS: TYPE I MEMBRANE PROTEIN.

CHIEFERNATIVE PRODUCTS: TWO ISOFORMS IN THE CYTOPLASMIC REGION ARE PRODUCED BY DIFFERENTIAL SPLICING.

CHAPTERNATIVE PRODUCTS: TWO ISOFORMS IN THE CYTOPLASMIC REGION ARE PRODUCED BY DIFFERENTIAL SPLICING.

CHAPTERNATIVE PRODUCTS: TWO ISOFORMS OF THREE X-LINKED SYNDROMES. 1: HYDROCEPHALUS OWING TO STENOSIS OF THE AQUEDUCT OF SYLVIUS (HSAS) CHARACTERIZED BY MENTAL RETARDATION AND BULARGED BY BRAIN VENTRICLES. 2: MASA SYNDROME WHICH IS CHARACTERIZED BY MENTAL RETARDATION, APHASIA, SHUFFLING GAIT, AND ADDUCTED THUMBS. HAS AN OVERLAPPING PROPILE OF CLINICAL SIGNS WITH HSAS, BUT WITH A MILDER PRESENTATION AND A LONGER LIFE EXPECTANCY. 3: SPASTIC PARAPLECIA TYPE 1 (SPG1), COLLECTIVELY THESE SYNDROMES ARE ALSO KNOWN AS CRASH SYNDROME, AN ACCOMYM WHICH STANDS FOR CORPUS CALLOSUM HYPOPLASIA, AND HYDROCEPHALUS.
                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. -!- DATABASE: NAME-LICAM; NOTE-LICAM mutation Web Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DISEASE: DEFECTS IN LICAM ARE THE CAUSE OF HIRSCHPRUNG DISEASE
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Hum. Mutat. 12:259-266(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS HSAS/MASA THR-219; ARG-335; CYS-386; CYS-473 AND LEU-1224
MEDLINE=98415726; Pubmed=9744477;
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Vits L., Chitayat D., van Camp G., Holden J.J.A., Fransen E.,
                                                                                                                                                                                          151 GESVVLPCNPPPSAEPLRIYW 171
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                     30.9%; Score 50; DB 42.9%; Pred. No. 29; tive 2; Mismatches
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Kobayashi M., Miura M., Asou H., Uya
"Molecular cloning of cell adhesion
tissue: a comparison of the primary
different origin.";
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Rathjen F.G.
"A human bra
                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics [6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A., Mackinnon R.N., Jones D.S. "PCR walking from microdissection clone from the human gene for the neural cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Last annotation update)
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
L1CAM OR CAML1 OR MIC5.
                             Fransen E.,
Willems P.J
                                         VARIANT HSAS/MASA LEU-1194.
MEDLINE-95187172; PubMed-7881431;
Fransen E., Schrander-Stumpel C.,
                                                                                                                                                                                                                   molecule
                                                                                                                                                                                                                                                                                                                                                             Stallcup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CAM-L1).":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reid R.A., Hemperly J.J.;
"Variants of human L1 cell
splicing of RNA.";
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Mammalia; Eutheria; Primates;
                                                                                                                                                          MEDLINE=94004956;
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                                                                                                                            4004956; PubMed=8401576; Rosenthal A., Macfarlane se mutation confirms the D
              hydrocephalus
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; PubMed=1993895;
nce J.T., Healy P.
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R., Mujoo K., S
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Eur. J.
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[19]
                                VARIANTS HSAS/MASA ASP-691; ARG-698 AND PRO-935.
MEDLINE-98180721; PubMed-9521424;
Du Y.-Z., Srivastava A.K., Schwartz C.E.;
"Multiple exon screening using restriction endonuclease "ingerprinting (REF): detection of six novel mutations adhesion molecule (LICAM) gene.";
Hum. Mutat. 11:222-230(1998).
                                                                                                                                                                                                                            VARIANTS HSAS Q-184; V-439--T-443 DEL; C-784 AND L-936--
MEDLINE-9738664; PubMed-9195224;
Macfarlane J.R., Du J.-S., Pepys M.E., Ramsden S., Donna
Charlton R., Garrett C., Tolmie J., Yates J.R.W., Berry
Moncla A., Lunt P., Hodgson S., Jouet M., Kenwrick S.;
"Nine novel LI CAM mutations in families with X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                         WARIANTS HSAS CYS-194 AND LEU-240
MEDLINE-97083370; PubMed-8929944;
Gu S.-M., Orth U., Veske A., Endet
Engel W., Schwinger E., Gal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jouet M., Moncla A., Paterson J., McKeown C., Holmberg E., Wadellus C., Kenwrick S.; "New domains of neural cell-adhesion molecule x-linked hydrocephalus and MASA syndrome."; Am. J. Hum. Genet. 56:1304-1314(1995).
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Winter R.M.,
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                                                                                                                                                                                                            hydrocephalus."
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MEDLINE=96057511; PubMed=7562969;
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Jouet M., Moncla !
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CRASH
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95004609; PubMed=7920660;
van Camp G., Coucke P., Fransen
E., Korn B., Poustka A., Wilson
M., Schwartz C., Willems P.J.;
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PRO-632
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PubMed=7762552;
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PubMed=7920659;
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              Hou S., Wohldmann P.;
Submilted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
                                                                                                                                       Malakooti J., Dahdal R.Y., Schmidt L., La
Ramaswamy K.;
"Molecular cloning, tissue distribution,
the human Na(+)/H(+) exchanger NHE2.";
Am. J. Physiol. 277:G383-G390(1999).
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MEDLINE-99375108;
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Pfam; PF00999; Na_H_Exchanger;
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SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON A
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Yu Y., Whitney R.G., Sato J.D.;
"Coding region for human VEGF receptor KDR (VEGFR-2).";
"Coding region for human VEGF receptor KDR (VEGFR-2).";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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HOMO Sapiens (Human).
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p35968; 060723; 014178;
01-JUN-1994 (Rel. 29, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC
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Yin L.Y., Wu Y., Patterson C.;

"Full length human KDR/flk-1 s
submitted (DEC-1997) to the EM
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Pfam; PF00047; ig; 6.

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SMART; SM00408; IGC2; 2.

SMART; SM00410; IG_Like; 4.

SMART; SM00210; TyrKC; 1.

SMART; SM00210; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

PROSITE; PS00211; PROTEIN_KINASE_DOM; 1.

Signal; Transferase; Tyrosine-protein kinase; Re
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Harber E.;
"Cloning a
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                                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
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6:1677-1683(1991).
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                                                                                                                                                                                                                                                                                                                                                                         : IPR000719; ; IPR003006; ; IPR003598;
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IPR003600; Ig_like.
IPR001824; Rcptor_tyr_kin_III.
IPR001245; Tyr_kin.
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Gene 104:329-333(1995).
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-i- FUNCTION: THE RECEPTOR BINDS POLYMERIC THE COMPLEX IS
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Immunoglobulin domain; Repeat;
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MEDLINE-96069604; PubMed-7590352;
Verbeet M.E., Vermeer H., Warmerdam G.
"Cloning and characterization of the b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L04797;
EMBL; X81371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO SECRETED. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AN SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: FOUND IN MAMMARY GLAND, JEJUNH, LUNG, KIDNEY AND SMALL INTESTINE.
FIN: IN THE ABSENCE OF DIMERIC IGA, SER-727 IS PHOSPHORYLATEI WHICH ALLOWS PIGR TO FUNCTION NORMALLY.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASOLATERAL SURFACE OF EPITHELIAL TRANSPORTED ACROSS THE CELL TO BE DURING THIS PROCESS A CLEAVAGE OCC EXTRACELLULAR (KNOWN AS THE SECRET TRANSPERBRANC SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003599; Ig.
IPR003006; Ig_MHC.
IPR003600; Ig_like
                                                                                                                       AAC41620.1; -.
CAA57136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
435
82434
   MW;
               COTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN 1.

IG-LIKE V-TYPE DOMAIN 2.

IG-LIKE V-TYPE DOMAIN 3.

IG-LIKE V-TYPE DOMAIN 5.

BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYMERIC-IMMUNOGLOBULIN RECEPTOR SECRETORY COMPONENT (BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; Signal; Alternative splicing.
DCED67FDD6A6E6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO BE SECRETED AT THE APICAL SURFACE.
AGE OCCURS THAT SEPARATE THE
SECRETORY COMPONENT) FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.C., de Boer H.A., Lee S.H.;
bovine polymeric immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATED
                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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RESULT 12
CAML_MOUSE
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Best Local Similarity
Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1989
01-OCT-1989
20-AUG-2001
NEURAL CELL A
                                                                                                                                                                                                        InterPro; IPR001777; I
InterPro; IPR003006;
InterPro; IPR003598;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAML_MOUSE P11627;
                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOOS M., Tacke R., Scherer H., Teplow D., Frueh Neural adhesion molecule L1 as a member of the superfamily with binding domains similar to fibr Nature 334:701-703(1988).

1 FUNCTION: CELL ADHESION MOLECULE WITH AN IMPOUNT OF THE MERVOUS SYSTEM. INVOLVED ADHESION, NEURITE EASCICULATION, OUTGROWTH C
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                  SMART; SM00060; FN3;
SMART; SM00408; IGC2
SMART; SM00410; IG_1:
                                                                                                                                                                    Pfam; PF00041; fn3; 4
Pfam; PF00047; ig; 6.
PRINTS; PR00014; FNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                  SIGNAL
                                                                                                                      Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                        HSSP; P20241; 1CFB.
MGD; MGI:96721; L1c
                                                                                                                                                                                                                                                                                EMBL; X12875
PIR; S05479;
                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=88318924; PubMed=3412448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 KNVTAWLGEPLKLSC
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                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: TWO ISOFORMS IN THE CYTOPLASMIC REGIC
PRODUCED BY DIFFERENTIAL SPLICING (BY SIMILARITY).
SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO AXONIN ON NEURONS
                                                                                                                                                                                                                                                                                            X12875; CAA31368.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.,
 1147
50
150
256
346
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20
1124
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(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
ADHESION MOLECULE L1 PRECURSOR (N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                 S05479.
                                                                                                            domain;
                                                                                                                                                                                                                                                         Licam
                                                                                                                                    IG_like;
                                                                                                                                               IGc2;
                                                                                                                                                                      FNTYPEIII.
  19
1260
1123
1146
1260
120
215
318
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                                                                                                                                                                                                      FN_III.
Ig_MHC.
Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.5%;
                                                                                                            Signal;
EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.
                                                                                                           Transmembrane;
l; Alternative s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teplow D., s a member o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260
                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Frueh K., Schac
r of the immunoglo
r to fibronectin.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                    ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AN IMPORTANT ROLE IN THE VOLVED IN NEURON-NEURON ROWTH OF NEURITES, ETC. BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (N-CAM
                                                                                                           splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h K., Schachner Me immunoglobulin bronectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 757;
                                                                                                                       Brain;
                                                                                                                                                                                                                                                                                                                                           bу
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                                                                                                                                                                                                                                                                                                                                                                               EMBL
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                                                                                                                                                                                                                                                                                                                                                                                         collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus.
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                                                                                                                                                                                                                                                                                                                                                                               outstation
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36

QVVTAVEYQEAILACKTPKKTVSSRLEWK

64

NRG1\_XENLA STAN
C93383; C9W6N0;
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4

40,

40,

Last sequence update)

XENLA

STANDARD;

PRT;

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RESULT FOR SULT FOR S
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                                                            EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., "Cloning of cDNAs encoding xenopus neuregulin: muscle during embryo development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM ALPHA1), AND MEDLINE-98352126; PubMed=9685585;
                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM CRD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99316087; PubMed=10383827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
                                             InterPro;
                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                    FORM.
                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: PROTEOLYTIC
                                                            ; AF076618; AAC;
; AF142632; AAD;
; Q02297; 1HRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Res. Mol. Brain Res. 58:59-73(1998).
                                                                                                                                            an email
                                                                                                                                            requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              EXTENSIVE GLYCOSYLATION PRECEDES
  IPR003006;
IPR003598;
                                           IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus.
                                                                               AAC26804.1;
AAD33893.1;
                                                                                                                                                                                                                                                                                                                               CONTAINS 1 EGF-LIKE DOMAIN CONTAINS 1 IMMUNOGLOBULIN-I
                                                                                                                                                                                                                                                                                                              BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 40, Last annotation update)
PRECURSOR (PRO-NRG1) [CONTAINS: NEUREGULIN-1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                       LEADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; E; Anura; Mesobatrachia; Pipoidea;
Ig_MHC.
Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE CLOSE TO
ADS TO THE RELEASE
                                         EGF-like
                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IS ELICITED
                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                   THE PLASMA MEMBRANE ON OF THE SOLUBLE GROWTH TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                              THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENTIRELY BY THE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                              PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                  C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.W.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE
                                                                                                                                                                                                                                                    a collaboration
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RESULT 11 PIGR_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
          DNA Cell
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID DISULFID DISULFID
                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING TISSUE-Small intestine, and Mammary gland; MEDLINE-95186063; PubMed-7880445; MISSER M.A., Krajci P., Myklebost O., Rogne Rulseth M.A., Krajci P., Myklebost O., Rogne
                                                                                                                                                                                   PHIGR_BOVIN STANDARD; PRT; 757 AA P81265; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) POLYMERIC - IMMUNOGLOBULIN RECEPTOR FRECURSOR [CONTAINS: SECRETORY COMPONENT].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
Pfam; PF02158; Neuregulin; 1
PRINTS; PR01089; NEUREGULIN
                   "Cloning and characterization of two forms immunoglobulin receptor cDNA."; DNA Cell Biol. 14:251-256(1995).
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                                                                          PIGR
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00181; EGF; 1
SMART; SM00408; IGc2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00022; EGF_1;
PROSITE; PS01186; EGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002154; Neuregulin
Pfam; PF00008; EGF; 1.
SEQUENCE FROM
                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Alternative splicing
                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                 GKKLVLKCQAVSEQPSLKFRW
                                                                                                                                                                                                                                                                                                                                      GEPLVLKCKGAPKKPPQRLEW
                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         677
                                                                                                                                                             (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
281
50
188
189
200
222
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
280
677
119
232
2116
206
220
231
130
134
                                                                                                                                                                                                                                                                                                                                                                                                                                               252
                                                                                                                                                                                                                                                                                                                                                                                                                        75794
                                                                                                                                                                                                                                                                                                                                                                        31.5%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE DOMAIN.
EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAEKKKVKEGKGRKGKGKKDRKGKKAEGSDQGAAASPKLKE
IKTQSYQEGKKLVLKCQAVSEQPSLKFRWFKGEKEIGAKNK
PDSKPEHIKIRGKKKSSELQISKASSADNGEYKCMYSNQLG
NDTYTVNVTIVPK -> MSEDTAEGLONGCSEQSSDPSAE
LQNEESMPETQDEEETTHGITGLAITCCVCLEADRLRICLN
                                                                                                                                                                                                                                                                                                                                                                                   Score 51;
                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        RCQNYVMASFYK (IN ISOFORM CRD).
49279E8F5BAE396F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              KPGFTGARCTETDPLRVVRSEKHLGIEFME
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKFGTSLLPTE (IN ISOFORM CRD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEKICIIPILACLISLCLCIAGLKWVFVDKIFEYDSPTHLD
PGHRGQDLILYTDTAPSTLVPSSVRTLPVIIPTTDSKAAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
INTERNAL SIGNAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-NEUREGULIN ALPHA1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUREGULIN ALPHA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                               rion update)
                                                      Rogne S.;
                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                           of bovine polymeric
                                                                                                                                                                                               (POLY-IG RECEPTOR) (PIGR)
                                                                                                                                                                                                                                                                                                                                                                                    Length 677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                       Euteleostomi;
cora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE - BOUND
                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              v
                                                                                                                                                                                                                                                                                                                                                            Gaps
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EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM.

PROTEOLYTIC

CLEAVAGE (BY

C2-TYPE DOMAIN

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                                                                                                     Matches
                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000561; EGF-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003154; Neuregulin.
Pfam; PF00047; Ig; 1.
Pfam; PF00047; Ig; 1.
Pfam; PF02158; Neuregulin; 1.
PFRNTS; PR01089; NEUREGULIN.
SMART; SM00181; EGF; 1.
SMART; SM00108; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                    VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF045654; AAC05670.1; -. EMBL; AF045655; AAC05671.1; -. EMBL; AF045656; AAC05672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROSIMILARITY).
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 IMMUNOSIOBULIN-LIKE C:
-i- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY
                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L11264; AAA49037.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane,
QNITARIGEPLVLKCKGAPKKPPQRLEW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q02297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor;
                                          Similarity
                                                                                                    406
                              Conservative
                                                                                                                                                388
                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                       1 Alternative splicing.
1 602 PRO-NEUR:
1 205 NEUREGUI.
1 206 INTERNACELI
207 229 INTERNAL
208 IG-LIKE (
209 CYTOPLASI
42 112 IG-LIKE (
200 SER/THR-:
201 136 SER/THR-:
201 149 105 BY SIMIL
201 155 BY SIMIL
201 180 BY SIMIL
201 180 BY SIMIL
201 180 BY SIMIL
201 N-LINKED
201 133 N-LINKED
201 126 NATISEGP
                                                                                                     AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like domain;
                                                                                                    602
67453
                                                                                                                                                405
                                         32.7%;
                                                                                                    WW;
                                                                                                                                                                                                                             BGF-LIKE
BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).
MWATISEGPLOYSLAPTOTIDNUSSYNTYPERLEKNKOEVAV
GOKLULACETTSEY PALAFEKULKUGEBIT KNURPENWKIPK
KOKKYSELHIYRATLADAGEYACRVSSKLGNDSTKASVIIT
DTNA -> MSEWGTETFPSPSAQLSDASLGGLASEKNEPG
PHREDSRYPGYAGASTGCVCLEAERLKGCLNSEKIGIAPI
LACLLSLCLCIAGLKWYFYDKIFEYDSPTHLDPGRIGGDPR
STVDPTALSAWVPSEVYASPEPIPSLESKAEVTOOTDSSLO
                            7;
                                                                                                  (IN ISOFORM BETA2B).
MISSING (IN ISOFORM BETA2B).
; 4183C0E56CE5D346 CRC64;
                                            Pred.
                                                                                                                                          MISSING (IN ISOFORM BETA2A AND ISOFORM BETA2B).
VSAMTTPARMSPVDFHTP -> HTPPTSLLLAGKVSLRVS
                                                                                                                                                                                       PSRPFLQPSLYNRILDVGLWSSATPSLSPSSLEPTTASQAQ
ATETNLQTAPKLS (IN ISOFORM BETA1A, ISOFORM
BETA2A AND ISOFORM BETA2B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERNAL SIGNAL SEQUENCE (POTENTIAL)
CYTOPLASMIC (POTENTIAL),
IG-LIKE C2-TYPE DOMAIN.
SER/THR-RICH.
                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUREGULIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Glycoprotein;
                                          No.
                                             ഗ
                                                         DB 1;
                            12;
                                                      Length 602;
                            Indels
                            0
                           Gaps
                            0
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N

l Similarity 12; Conser

Conservative

Ψ

Mismatches

14;

Indels

0;

Gaps

0

QNITARIGEPLVLKCKGAPKKPPQRLEWK

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Query Match
Best Local s
Matches 12
                                                                     CARBOHYD
SEQUENCE
                                                                                                            DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells.";

J. Biol. Chem. 275:19139-19145(2000).

-i- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING SECONDARY LYMPHOID ORGANS.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).

-i- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.

LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                          Immunoglobulin
SIGNAL 1
                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JAM).
                                                                                                CARBOHYD
                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF255910; AAF81223.1;
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Vascular endothelial cells; MEDLINE=20317114; PubMed=10779521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P57087;
20-AUG-2001
                                                                                                                                                           DOMAIN
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
"Vascular endothelial junction-associated molecule, a novel member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C210RF43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEJA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 KNQEVAVGQKLVLRCETTSEYPALRFKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                IPR003600;
                                                                                                                                                          21
239
260
43
148
                                                                                                                                                                                                                                                                         domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                               238
259
298
116
221
109
214
98
187
236
33207
                                                                                                                                                                                                                                             20
298
                                                                                                                                                                                                                                                                                                                                ; Ig_MHC.
; Ig_c2.
; Ig_like.
             32.1%;
                                                                                                                                                                                                                                                                       Glycoprotein; Transmembrane; Signal
                                                                       ₹.
                                                                    POTENTIAL.

N-LINKED (GLCNAC. . .) (PO
             Score 52;
Pred. No.
                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               MOLECULE.
                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED
                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
           DB 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                          ۲.
                         Length 298
                                                                                                 .) (POTENTIAL).
.) (POTENTIAL).
                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO
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RX MEDLINE-9221111; PubMed-1313497;
RA POURQUIE O., Hallonet M.E.R., le Douarin N.M.;
RT "Association of BEN glycoprotein expression with climbing fiber RT axonogenesis in the avian cerebellum.";
RL J. Neurosci. 12:1548-1557(1992).
C. -- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING C.-- FUNCTION: TOMOPHILIC ADHESION EXTENSION.
C. -- FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
C. -- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
C. -- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED TO AXONS IN THE DORSAL C. TUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN C. EPUTHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOLETIC CELLS. EACH DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS C. OF BEN.
                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
CARBOHYD
CONFLICT
CONFLICT
                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a or send an email +~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                       CARBOHYD
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "BEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pourquie O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92302224; PubMed=1608932;
                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENT.
SIMILARITY: E
3 C2-LIKE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $63276; AAB20170.1; -. M76678; AAA48602.1; -. X64301; CAA45579.1; -. Q13740; 1KJC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2-LIKE AND 2 V-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00410; IG; 3.
SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e O., Corbel C., le Caer J.-P., Rossier J., surface glycoprotein of the immunoglobulin ed in a variety of developing systems.", atl. Acad. Sci. U.S.A. 89:5261-5265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00290; IG_MHC;
  42 > 156 | 269 | 352 | 352 | 433 | 443 | 163 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 312 | 3
FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN 1.

IG-LIKE V-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                         EPPSRRRP
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(POTENTIAL).
(POTENTIAL).
) (POTENTIAL).
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ARIA, a protein that stimulates acetylcholine receptor a member of the neu ligand family."; Cell 72:801-815(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                     DOMAIN CONTAINING ISOFORMS (CRD-NRG) PROBABLY REGULATE THE EXPRESSION OF NICOTINIC ACETYLCHOLINE RECEPTORS AT DEVELOPING INTERNEURONAL SYNAPSES. THE IG-NRG ISOFORM IS REQUIRED FOR THE INTIAL INDUCTION AND/OR MAINTENANCE OF THE MATURE LEVELS OF ACETYLCHOLINE RECEPTORS AT NEUROMUSCULAR SYNAPSES.

-IS SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A PROTECLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

-I- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; ARIA/IG-NRG (SHOWN HERE), CRD-NRG-BETALA, CRD-NRG-BETALA AND CRD-NRG-BETALA, REPRODUCED BY ALTERNATIVE SPLICING. ARIA CONTAINS AN IG-LIKE DOMAIN WEDEREAS IN THE CRD-NRG (OR NARIA) ISOFORMS; THE EGF-LIKE DOMAIN IS REPLACED BY A CYSTELMS-RICH DOMAIN (CRD).

-I- DEVELOPMENTAL STAGE: CRD-NRG ISOFORM IS DETECTED AT EMBRYONIC DAY 4 (ED4) IN BOTH VISCERAL AND SOMATIC MOTOR NEURONS OF SPINAL CORD AND IS HIGHEST AT ED5. IG-NRG ISOFORM IS NOT EXPRESSED UNTIL ED 6 IN SPINAL CORD. AT ED 11 BOTH ISOFORMS DISPLAY COMPARABLE LEVELS.

-I- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHICK
                                                                                                                                                                                                                                                                                                                                                                                     Yang X., Kuo Y., Devay P., Yu C., Role L.;
"A cysteine-rich isoform of neurgulin con
expression of neuronal nicotinic receptor
synaptogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q05199; 073750; 073751; 073752;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PRO-NBUREGULIN-1 PRECURSOR (PRO-NRG1) [CONTAINS:
(ACETYLCHOLINE RECEPTOR INDUCING ACTIVITY) (ARIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRG1_CHICK S
Q05199; 073750;
20-AUG-2001 (ReJ
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                                                                                                                                                                                                                                                                                                                                                            Neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACETYLCHOLINE RECEPTOR NRG1 OR ARIA.
                                                                                      -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS BETA1A; BETA2A TISSUE-Brain, and Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WHITE LEGHORN;
MEDLINE-93201602; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98150951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 SQSSTIKEGDNVTLKCSGNGNPPPQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQNITARIGEPLVLKCKGAPKKPPQ
                                                                                                                                                                                                                                                                                                                                            FUNCTION: DIRECT LIGAND FOR THE ERBB TYROSINE KINASE RECEPTORS THE MULTIPLE ISOFORMS PERFORM DIVERSE FUNCTIONS: CYSTEIN-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9491987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM ARIA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neognathae;
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329
402
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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                            BINDING
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Pred. No.
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                             ENTIRELY BY THE EGF-LIKE
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PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE

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RESULT 6
FYB MOUSE
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DT 15-JU
DT 20-AU
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DT 20-AU
DT 20-AU
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DT 15-JU
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DT 20-AU
RY-B
GN FYB.

OS FYN-B
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OC MAMMAA
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                                                                                                                                                                                                                                  NAME MOREOUS C.C., Rudd C.E.;

"Novel isoform of lymphoid adaptor FYN-T-binding protein (FYB-130)

"Interacts with SLP-76 and up-regulates interleukin 2 production.";

"Interacts with FYN AND SLP-76 and SH2-DOMAIN-C CONTAINING LEUCOCYTE PROTEIN-76 (SLE)-76) SIGNALING CASCADES IN TOCK CONTAINING LEUCOCYTE PROTEIN-76 (SLP-76) SIGNALING CASCADES IN TOCK COLLES, MODULATES THE EXPRESSION OF INTERLEUKIN-2 (IL-2).

"Interacts with FYN AND SLP-76.

"Interac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYB_MOUSE STANDARD; FALL, C.1.

935601; Q922H3;

15-UUL-1999 (Rel. 38, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
FYN-BINDING PROTEIN (FYN-T-BINDING PROTEIN) (FYB-120/130) (P120/P130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=T-cell lymphoma;
TISSUE=T-cell lymphoma;
MEDLINE=97352826; PubMed=9207119;
da Silva A.J., Li Z., de Vera C., Canto E., Findell P., Ru
da Silva A.J., Li Z., de Vera C., Canto E., Findell P., Ru
"Cloning of a novel T-cell protein FYB that binds FYN and
"Cloning of a novel T-cell protein 76 and modulates interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 99428514; PubMed=10497204;
Veale M., Raab M., Li Z., da Silva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISC
TISSUE=T-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                 PHOSPHORYLATION SIMILARITY: CONT
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4; Mismatches
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Best Local
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD166 ANTIGEN PRECURSOR (SC1 GLYCOPROTEIN) (BEN GLYCOPROTEIN) (DM-
GRASP PROTEIN) (JC7 PROTEIN).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
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VARSPLIC
SEQUENCE
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SEQUENCE FROM N.A., AND SEQUENCE TISSUE=Bursa of fabricius;
                                        Neuron
[3]
                                                     "DM-GRASP, a novel immunoglobulin that supports neurite extension."; Neuron 7:209-220(1991).
                                                                                                                                                                                                       Tanaka H., Matsui T., Agata A., Tomura M., Kubota I., McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton "Molecular cloning and expression of a novel adhesion mc Neuron 7:535-545(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C166_CHICK
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                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=91337449; PubMed=1873027;
                                                                                                                                                                                                                                                                                MEDLINE=92030150;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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1 Genes Dev. 7:1471-1484(1993).

C -!- FUNCTION: PROBABLE ROLE IN MYOFILAMENT ASSEMBLY AND/OR ATTAC
C -!- FUNCTION: PROBABLE ROLE IN ERCEPTORS IN MUSCLE.

OF THE MYOFILAMENT LATTICE TO THE CELL MEMBRANE. UNC-52 MAY
EXTRACELLULAR ANCHOR FOR INTEGRIN RECEPTORS IN MUSCLE.

C -!- SUMCELLULAR LOCATION: EXTRACELLULAR MATRIX.

C -!- SUMCELLULAR LOCATION: EXTRACELLULAR MATRIX.

C -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANE OF ALL
CONTRACTILE TISSUES. IT IS CONCENTRATED OVER MUSCLE DENSE BOOM AND M-LINES WHICH ARE ASSOCIATED WITH BETA-INTEGRIN.

C -!- DEVELOPMENTAL STAGE: SYNTHESIZED EARLY IN EMBRAOGENESIS.

-!- SIMILARITY: CONTAINS 3 LDL-RECEPTOR CLASS A DOMAINS.

C -!- SIMILARITY: CONTAINS 7 LAMININ EGF-LIKE DOMAINS.

C -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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01-JUN-1994 (Rel. 2
15-JUL-1999 (Rel. 3
BASEMENT MEMBRANE F
                                     InterPro;
Pfam; PF00
Pfam; PF00
Pfam; PF00
Pfam; PF00
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions use modified and this statement is not removed.
modified and this statement is not removed.
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entities requires a license@isb-sib.ch).
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Q06561;
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InterPro;
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MEDLINE=93339574; PubMed=8393416;

MEDLINE=93339574; PubMed=8393416;

Rogalski T.M., Williams B.D., Mullen G.P., Moerman D.G.;

"Products of the unc-52 gene in Caenorhabbitis elegans are homologous to the core protein of the mammalian basement membrane heparan
                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the property of the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNITARIGEPLMLSCKGAPKKPTQKLEWK 52
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                                       PF00053;
PF00057;
                                                                                                                                                                                                                                                                                                        L13458; AAA28156.1; P01130; 1AJJ.
                                                                                   PF00052;
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                    PD003031;
                                                                                                                          : IPR002172; I
: IPR000034; I
: IPR002049; I
: IPR000519; I
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IPR003006;
IPR003598;
IPR003600;
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           laminin_B; 2.
laminin_EGF; 5
ldl_recept_a;
ldl_raminin_B;
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Ig_c2.
Ig_like.
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Pred. No. 2
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594481BC3A51E94E CRC64;
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http://www.isb-sib.ch/announce/
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                  SMART; SM00180; EGF_Lam; 5.

SMART; SM00408; IGC2; 11.

SMART; SM00401; IG_like; 5.

SMART; SM00281; LamB; 2.

SMART; SM00018; P; 1.

PROSITE; PS00022; EGF_1; 4.

PROSITE; PS00186; EGF_2; 2.

PROSITE; PS01209; LDLRA_1; 3.

PROSITE; PS01209; LDLRA_1; 3.

PROSITE; PS01209; LDLRA_1; 3.

PROSITE; PS01248; LAMININ_TYPE_EGF; 7.

PROSITE; PS01248; LAMININ_TYPE_EGF; 7.

PROSITE; PS01248; LAMININ_TYPE_EGF; 7.

PROSITE; PS0126; Extracellular matrix; Allerials
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IG-LIKE C2-TYPE DOMA
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LDL-RECEPTOR CLASS P
LDL-RECEPTOR CLASS P
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
IG-LIKE C2-TYPE DOMAIN 2.
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trix; Alternative splicing;
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SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. Tuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycosylation end products of proteins.";
J. Biol. Chem. 267:14998-15004(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neeper M., S
Elliston K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung;
MEDLINE=92340547; PubMed=1378843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                CARBOHYD
                                                                                  DISULFID
                                                                                                       DISULFID
                                                                                                                           DISULFID
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M91212; AAA03575.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and expression of a cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGER OR RAGE
                                                                                                                                                                                                                                                                                                                                   mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATE IN DIABETES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOL. Chem. 267:14998-15004(1992).
FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
PRODUCTS (AGE). THESE ARE NONEWZYMATICALLY GLYCOSYLATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH ACCUMULATE IN VASCULAR TISSUE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNITARIGEPLVLKCKGAPKKPPQRLEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Swiss Institute of Bioinformatics and the EMBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt A.M., Brett ., Stern D., Shaw A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   ; £4;
                                                                                                                                                                                                                                                                                                                                   domain; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos
                       352
373
416
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213
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    44182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE
  MW;
                            POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

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OTENTIAL
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                       POLY-GLU
                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.,
B703815573E767AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yan S.D., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
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                                                                                                                                                                                                                                                                         GLYCOSYLATION END PRODUCT-
RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGING AND AT AN ACCELERATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              advanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAGE_RAT
                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAT
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTO
(RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                               DOMAIN
                                                                                                        DOMAIN
                                                                                                                              CHAIN
                                                                                                                                                                                               Pfam; PF00047; ig;
                                                                                                                                                                                                           InterPro; IPR003006;
InterPro; IPR003598;
InterPro; IPR003600;
                                                                                                                                                                                                                                             EMBL; L33413; AAA42027.1;
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                              MO1. Pharmacol. 52:54-62(1997).
-i- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renard C., Chappey O., Wautier M.P., Nagashima M., Lu
Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wa
"Recombinant advanced glycation end product receptor
in normal and diabetic rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE=Lung; MEDLINE-97368045; PubMed=9224812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                          DOMAIN
                                                                                             TRANSMEM
                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGER OR RAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                     [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN TISSUE SPECIFICITY: ENDOTHELIAL CELLS. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                        RATE IN DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                   WHICH ACCUMULATE IN VASCULAR TISSUE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNITARIGEPLVLKCKGAPKKPPQRLEWK
                                                                                                                                                                                                                                                                                                                                                           C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                        SM00408; IGC2; 1.
SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
26; Conser
                                                                                                                                                               PS00290;
 23
342
363
31
136
250
250
257
257
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                                                                                                                                                     domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, Created)
35, Last seq
                                                                                                                                                               IG_MHC;
 341
362
402
105
212
306
98
206
299
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402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia;
                                                                                                                                                                                                           Ig_c2.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.5%;
                                                                                                                                                                                                                                 Ig_MHC.
                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 145; DB 1;
Pred: No. 3.5e-13;
2; Mismatches 1;
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. .
                                                                                                     ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                              IG-LIKE V-TYPE DOMAIN. IG-LIKE C2-TYPE DOMAIN IG-LIKE C2-TYPE DOMAIN
                                                                               CYTOPLASMIC
                                                                                             POTENTIAL.
                                 POTENTIAL.
                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                   Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402
                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   AGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                         SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                    AND
.) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lundh E.,
Wautier J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                    ΑT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmacokinetics
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                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                             collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                           n no way
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Query Match
Best Local
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M91211; AAA03574.1; -. EMBL; D28769; BAA05958.1; -. EMBL; U89336; AAB47491.1; -. EMBL; AB036432; BAA89369.1; -. EMBL; AJ133822; CAB43108.1; -. EMBL; AF208289; AAG35728.1; -.
                                                                                                                                                                         CARBOHYD
DOMAIN
VARSPLIC
                                                                                                                                                                                                                      DISULFID DISULFID DISULFID
                                                         CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                Piam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRU Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/RAGESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end-products (RAGE) gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Novel polymorphisms
                                                                                            VARIANT
                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RATE IN DIABETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2-LIKE AND ONE V-LIKE DOMAINS.
  30;
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003006;
                                                          404
  Conservative
                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Futers T.S.;
                                                                                                                                                                                                                                                                                                                                                                          domain;
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                                                                                                                                                                                                                                                                                                                                                                                       IG_MHC; 1
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363
404
106
214
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81
384
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig_MHC.
Ig_c2.
Ig_like.
                                                          42802
          100
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                                                                                                                                                                                                                                                                                                                                                                ; Glycoprotein; Transmembrane; Signal;
Polymorphism.
            .0%;
                                                          MW;
 0;
                                                                                                                                                                                              POLY-GLU.
Score 162; I
Pred. No. 1.3
); Mismatches
                                                                    Z
                                                                                                                                                                                                                                             IG-LIKE V-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
POTENTIAL.
                                                                                           GACRTESVGGT
Q -> R.
                                                                                                           ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIKAGNSS
PGPGDPGRPGSSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
                                                                                                                                                  GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRA VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAAL
                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                           LIGVILWQRRQRRGEERKAPENQEEEEEERAELNQSEEPEAG
ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
                                                                                                                                                                                                                                                                                                                              ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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                                                                               /FTId=VAR_011338
                                                        -> G (IN REF. 1)
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DB 1;
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s 0;
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AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30

Query Match Best Local Similarity

92.0%; 93.1%;

Score Pred.

149; DB 1; No. 9.1e-14;

Length 403;

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RASELUT 2
RAGE_MOUSE
ID RAGE_MOUSE
ID RAGE_MOUSE
ID RAGE_MO
COLUMN
DT 01-NOV
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Pfam; PF00047; 1g; 3.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                         TRANSMEM
DOMAIN
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,
Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
"Recombinant advanced glycation end product receptor pharmacokinetics
in normal and diabetic rats.";
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Mammalia; Eutheria;
NCBI_TaxID=10090;
    SEQUENCE
                                                                                                                                                              DOMAIN
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InterPro; IPR003598;
InterPro; IPR003600;
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                                                                                                                                        DOMAIN
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ENDOTHELLAL CELLS.
TISSUE SPECIFICITY: ENDOTHEL IMMUNOGLOBULIN SUPERFAMILY. CONTAINS SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
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  ΑA;
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Rodentia;
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Ig_like.
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                CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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Sciurognathi;
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Title: Perfect score:

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Scoring table:

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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
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162
1 AQNITARIGEPLVLKCKGAPKKPPQRLEWK 30
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Copyright (c) 1993 - 2000 Compugen Ltd
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                 RAGE_HUMAN
RAGE_MOUSE
RAGE_RAT
UN52_CAEEL
FYB_MOUSE
C166_CHICK
NRG1_XENLA
PIGR_BOVIN
NRG1_XENLA
PIGR_BOVIN
CAML_HUMAN
NAH2_HUMAN
CAML_HUMAN
CAML_RAT
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ICP4_
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Q15109 homo sapien Q62151 mus musculu Q28173 bos taurus Q63495 rattus norv Q06561 caenorhabdi Q55601 mus musculu P4229 gallus gall p57087 homo sapien Q9383 xenopus lae P81265 bos taurus P11627 mus musculu P3596 homo sapien Q0595 rattus norv P28925 equine herp P32064 homo sapien Q05695 rattus norv P4468 haemophilus Q73895 gallus gall Q01973 homo sapien P20741 drosophila Q91974 gallus gall Q01973 homo sapien Q05695 rattus norv P44686 haemophilus Q73895 gallus gall Q01973 homo sapien P20741 drosophila Q91044 gallus gall Q01973 homo sapien Q90718 gallus gall Q01973 homo sapien Q90718 gallus gall Q11931 homo sapien Q10718 gallus gallus gall Q11931 homo sapien Q10718 gallus gal
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2 gallus gall
9 homo sapien
1 homo sapien
1 homo sapien
1 homo sapien
2 rattus norv
8 equine herp
10 escherichia
9 rattus norv
8 haemophilus
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Result

Score

Query Match

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	P16843 huma	P12689 sacc	P40236 schi	P29294 oryc	P70699 mus	Q9z138 mus	Q01974 homo	P97333 mus	035136 mus	P34082 dros	035569 ratt	P34083 dros	
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## ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORM 2). Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; "CDNA cloning of a novel secreted isoform of the human Receptor for Advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. [6] SEQUENCE OF 1-12 FROM N.A.	FROM N.A., Dankers C., Spies T., G. (FEB-1997)  FROM N.A., J., Yoneku H., H., Sar heterogects.";	SEQUENCE FROM N.A. (ISOFORM 1).  MEDLINE-95137587; PubMed=7835890;  Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  Inoko H., Ikemura T.;  "Three genes in the human MHC class III region near the junction with  the class II: gene for receptor of advanced glycosylation end  products, PBX2 homeobox gene and a notch homolog, human counterpart  of mouse mammary tumor gene int-3.";  Genomics 23:408-419(1994).	rimates; Catarrhini; Hominidae; SOFORM 1).  SOFORM 1).  Med=1378843; M., Brett J., Yan S.D., Wang F. Shaw A.; on of a cell surface receptor f ducts of proteins."; 998-15004(1992).	UMAN  AGE_HUMAN  STANDARD;  15109; Q15279; Q9Y3R3; Q9H2X7  1-NOV-1997 (Rel. 35, Last sec  0-AUG-2001 (Rel. 35, Last and  DVANCED GLYCOSYLATION END PRO  RECLEPTOR FOR ADVANCED GLYCOSY  GER OR RAGE.  OMO Sapiens (Human).  Wetaroa: Chordata:

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Result
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3: sp_fungi:*
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Copyright (c) 1993 - 2000 Comp
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Q9V4J9
                                                                            Q9NBA1
Q9V787
                Q9U2F2
                         09вув8
                                                                                                                                                                          ㅂ
                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (without alignments)
69.720 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                        473505
                      092626 homo sapien
025198 hydra atten
092214 mus musculu
09uf14 homo sapien
09byb8 homo sapien
                                                                                                   O9trq1 bos taurus
O9xtd2 caenorhabdi
O18263 caenorhabdi
O9xt15 caenorhabdi
O9v4y0 drosophila
                                                          Q9v787
Q9n5c2
Q92626
                                                                                   Q9v4j9
Q9nba1
                Q9u2f2
                                                                                                                                                      Q9y3r3 homo sapien
                                                                                                                                                                        Description
                                                                                                                                               035444 mus musculu
                                                                 0 drosophila
9 drosophila
1 drosophila
7 drosophila
2 caenorhabdi
       caenorhabdi
drosophila
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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	<u>ω</u>	30	29	28	27	26	25	24	23	22	21	20
49.5	49.5	50 .	50	50	50	50	50	50	50	50	50	50	50.5	50.5	50.5	51	51	51	52	52	52	52	52.5	53	53
30.6	30.6	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	31.2	31.2	31.2	31.5	31.5	31.5	32.1	32.1	32.1	32.1	32.4	32.7	32.7
968	921	1259	1252	1252	1234	1154	538	392	386	377	372	284	1114	793	212	1442	455	305	1793	298	181	99	7962	1651	1651
ഗ	11	11	11	11	1,1	ω	11	N	10	u	7	N	4	11	10	12	4	7	ഗ	11	11	10	4	11	4
Q9VCM6	Q9QX38	Q9QY38	Q9JIX2	Q9QXX7	Q9R044	Q9P6W3	Q9QYQ7	Q9K6C8	004645	Q9VHR0	Q31406	Q9I452	Q9BWV1	070246	Q9FGP8	042066	Q9UIRO	098261	Q9NKJ4	Q9JI59	Q9CWD9	Q9FR57	Q10465	055005	Q9Y6N7
Q9vcm6 drosophila		Q9qy38 mus musculu	Q9jix2 rattus norv	Q9qxx7 rattus norv	Q9r044 rattus norv	Q9p6w3 neurospora	Q9qyq7 mus musculu	Q9k6c8 bacillus ha	004645 arabidopsis	Q9vhr0 drosophila	Q31406 gallus gall	Q9i452 pseudomonas	Q9bwv1 homo sapien	070246 mus musculu	Q9fgp8 arabidopsis	O42066 equine herp	Q9uir0 homo sapien	098261 homo sapien				Q9fr57 lycopersico	Q10465 homo sapien	O55005 rattus norv	Q9y6n7 homo sapien

## ALIGNMENTS

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Signal;
                                                                  Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like;
                                                                                                                                                                                                  Maiherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G., Schuler A., Huber G., "CDNA cloning of a novel secreted isoform of the human Receptor for Advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y3R3;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                             InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                         DOMAIN.
EMBL; AJ133822; CAB43108.1; -.
SEQUENCE
                                                                                                                                                                                        -!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               RAGESEC
                                                      Receptor.
342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                            1
23
                            22
342
36193 MW;
             POTENTIAL.
RECEPTOR FOR ADVANCED GLYCATION PRODUCTS.
35DDF66A13E39B38 CRC64;
                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
                                                                                                                                                                                        MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                      HISTOCOMPATIBILITY COMPLEX
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Query Match 100.0%; Score 162; DB 4; Best Local Similarity 100.0%; Pred. No. 5.1e-16; Matches 30; Conservative 0; Mismatches 0;

Length 342; Indels

0;

Gaps

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AQNITARIGEPLVLKCKGAPKKPPQRLEWK

AQNITARIGEPLVLKCKGAPKKPPQRLEWK

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23

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RESULT
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Best Local S
Matches 27
                        Query Match
Best Local 9
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TRQ1;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035444
035444;
01-JAN-1998
01-JAN-1998
01-JUN-2001
                                                                                                        MEDLINE=92340546; PubMed=1321822; Schmidt A.M., Vianna M., Gerlach M., Brett J., Ryan J., Kao J., Esposito C., Hegarty H., Hurley M., Clauss M.; "Isolation and Characterization of two binding proteins for advanced glycosylation end products from bovine lung which are present on the endothelial cell surface."; SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 402 AA; 42653 MW; DBFDC
                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Pfam; PF00047; 1g; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Rowen L., Mahairas G.,
Loretz C., Schmidt S.,
Submitted (OCT-1997) to
                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9TRQ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF030001; AAB82007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNITARIGEPLVLKCKGAPKKPPQRLEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNITARIGEPLVLSCKGAPKKPPQQLEWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Conservative
    22;
                                                                                                   . Chem. 20,
E 32 AA;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.) (TrEMBLrel.)
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                   Bos.
                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig_c2.
Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Qin S., Ahearn M.E., Dankers C., ., Tipton S., Traicoff R., Zackrone to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
93.1%;
                        75
                        . 78;
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05,
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 149; DE Pred. No. 5.1e
1; Mismatches
Score 108; DB 6;
Pred. No. 4.7e-09
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DBFDC50A6C8CB902 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
.le-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             β
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    5.
                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN (FRAGMENT).
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lasky S.,
K., Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402;
  0;
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  Gaps
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Best Local Similarity

50

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Score Pred.

NO .

DB 1.2;

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Length 2295

Query Match

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RESULT
Q9XTD2
  A COCOCOCAR RANGO O COCOCAR RANGO COCOCOCAR RANGO COCOCAR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000561; EGF-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000034; Laminin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 293395; CAB07707.1;
EMBL; 293375; CAB07768.1;
EMBL; 293375; CAB07568.1;
EMBL; 293375; CAB07568.1;
EMBL; 293395; CAB07568.1;
HSSP; P01130; 1LDR.
WormPep; 2C101.2C; CE15034
                                                           PROSITE; PS00022; E
PROSITE; PS01186; E
PROSITE; PS01248; I
PROSITE; PS01209; I
PROSITE; PS50068; I
PROSITE; PS00215; M
                                                                                                                                                                                                                                            ProDom; PD003031; I
SMART; SM00180; EGI
SMART; SM00408; IGG
SMART; SM00410; IG
SMART; SM00281; Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DATES C.;

Percy C., Baynes C.;

Percy C., Baynes C.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

-i- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A (01826-

-i- ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (SHOWN HERE)

TOOTORM ZC101.2E (09XT15); MAY BE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XTD2;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNC-52 PROTEIN.
UNC-52 OR ZC101.2.
Alternative splicing; EGF-like domain; Glycoprotein; Hypothetical protein; Laminin EGF-like domain; RepeaseQUENCE 2295 AA; 251087 MW; F6BC6067ABF86C48 CR
                                                                                                                                                                                                                                                                                                                                                                                                 pfam; PF00047; ig; 14.
pfam; PF00052; laminin_B; 2.
pfam; PF00053; laminin_EGF;
pfam; PF00057; ldl_recept_a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002172;
InterPro; IPR001993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LDLRA) DOMAIN
                                                                                                                                                                                   T; SM00192; LDLa; 3.

'; SM00018; P; 1.

TE: PS00000
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                                                                                                                                                                                                                                                                                                                                                        PR00011; EGFLAMININ. PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peloderinae;
                                                                                                                                                                                                                                                                                        EGF_Lam;
: IGc2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                 laminin_EGF; 5
ldl_recept_a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2C; CE15034
                                                                                                                                                                                                                                                                 IG_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OI
                                                                                    ; EGF_1; UNKNOWN_4.
; EGF_2; 2.
; LAMININ_TYPE_EGF; ; LDLRA_1; 3.
; LDLRA_2; 3.
                                                                MITOCH_CARRIER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                   Laminin_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOT
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Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DENSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12,
12,
17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
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ω
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPOPROTEIN
  F-like domain; Repeat.
F6BC6067ABF86C48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR CLASS
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HERE) AND
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                Query Match
Best Local
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     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 29335; CAB07706.1; --
EMBL; 293375; CAB07706.1; JO
EMBL; 293375; CAB07567.1; --
EMBL; 293375; CAB07567.1; JO
EMBL; 293395; CAB07567.1; JO
HSSP; P01130; 1LDR.
WormPep; ZC101.2A; CE15028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   018263;
01-JAN-1998 (TrEMBLrel. C
01-NOV-1998 (TrEMBLrel. C
01-JUN-2001 (TrEMBLrel. 1
UNC-52 PROTEIN.
UNC-52 OR ZC101.2.
                                                                                                                                                                                                                               ProDom;
SMART; S
SMART; S
SMART; S
SMART; S
SMART; S
SMART; S
                                                                            SMART; SMO0018; P; 1.

PROSITE; PS00022; EGF_1; UNKNOWN_4.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01248; LAMININ_TYPE_EGF; 7.

PROSITE; PS01209; LDLRA_1; 3.

PROSITE; PS01209; LDLRA_2; 3.

PROSITE; PS01205; LDLRA_2; 3.

PROSITE; PS02015; MITOCH_CARRIER; UNKNOWN_1.

Alternative splicing; EGF-like domain; Glycoprotein; Alternative splicing; EGF-like domain; Repeat SEQUENCE 2482 AA; 270943 MW; B24096F7DB694D70 CR0
                                                                                                                                                                                                                                                                                                                                                            Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percy C., Baynes C.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-i- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A (SHOWN HERE)

ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (Q9XTD2) AND ISOFORE

ZC101.2E (Q9XT15); MAY BE PRODUCED BY ALTERNATIVE SPLICING.

-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   018263
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                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LDLRA) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGEPLQVKCEAFGAPGDPEPEVEW
                                                                                                                                                                                                                                                                                                                                            PF00052;
PF00053;
PF00057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGEPLVLKCK--GAPKKPPQRLEW
                                                                                                                                                                                                                                          n; PD003031;
SM00180; EG;
SM00408; IG;
SM00410; IG;
SM00281; La;
SM00192; LD
l Similarity
12; Conserv
                                                                                                                                                                                                                                  SM00018;
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IPR000034;
IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000561; EGF-like.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                      IPR002172; LDL_recept_A.
IPR001993; Mitoch_carrier.
IPR000519; P_trefoil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                     ; laminin_EGF; 5.
; ldl_recept_a; 3.
731; Laminin_B; 2.
; EGF_Lam; 5.
                                                                                                                                                                                                                                                                            EGF_Lam; 5.
; IGc2; 11.
; IG_like; 5.
                                                                                                                                                                                                                                            LamB; 2.
LDLa; 3.
                                                                                                                                                                                                                             P; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematoda;
                39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminin_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig_MHC.
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08,
17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
 4:
                Score 64; I
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
 Mismatches
                                                                               F-like domain; Repeat
B24096F7DB694D70 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR HISTOCOMPATIBILITY COMPLEX
                                DB
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                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6,
 6;
                              Length 2482;
                                                                               CRC64;
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 Indels
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Gaps
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1;
                              RESULT
Q9XTI5
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Ω
R SMART; SM00192; LDLa; 3.

R SMART; SM00018; P; 1.

R PROSITE; PS00022; EGF_1; UNKNOWN_7.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01248; LAWININ TYPE_EGF; 7.

R PROSITE; PS01209; LDLRA_1; 3.

R PROSITE; PS01209; LDLRA_2; 3.

R PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.

M Alternative splicing; EGF-like domain; Glycoprotein; WHypothetical protein; Laminin EGF-like domain; Repeat.

M Hypothetical protein; Laminin EGF-like domain; Repeat.

SEQUENCE 3375 AA; 369049 MW; 1AA418BB4E5D67AA CRC64;
                                                                                                                                                                                                                                                                                                        InterPro; [PR001791; Laminin_G. InterPro; [PR002172; LDL_recept_A InterPro; [PR002172; MILC_recept_A InterPro; [PR001993; Mitoch_carrivInterPro; [PR001993; Mitoch_carrivInterPro; [PR001993; Mitoch_carrivInterPro; [PR000519; P_trefoil. Pfam; PF00047; 14; 17.

Pfam; PF00054; laminin_G; 2.
Pfam; PF00054; laminin_G; 2.
Pfam; PF00054; laminin_G; 2.
Pfam; PF00057; Idl_recept_a; 3.
PRINTS; PR00251; LDLRECEPTOR.
PRODOM; PF0003031; Laminin_B; 2.
SMART; SM00180; EGF_Lam; 5.
SMART; SM001001; EGF_Like; 3.
SMART; SM000408; IGC2; 12.
SMART; SM000408; IGC2; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (Tr
01-JUN-2001 (Tr
UNC-52 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003598;
InterPro; IPR003600;
InterPro; IPR003006;
InterPro; IPR000034;
InterPro; IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percy C., Baynes C.;

Percy C., Baynes C.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

-i- ALTERNATIVE PRODUCTS: FOUR FORMS; ISOFORM ZC101.2A (09XTI5),

-ISOFORM ZC101.2B (018261), ISOFORM ZC101.2C (09XTD2) AND ISOFORM ZC101.2E (SHOWN HERE); MAY BE PRODUCED BY ALTERNATIVE SPLICING.

ZC101.2E (SHOWN HERE); MAY BE PRODUCED BY ALTERNATIVE COMPLEX

-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNC-52 OR ZC101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XTI5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1990 VGEPLQVKCEAFGAPGDPEPEVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 IGEPLVLKCK--GAPKKPPQRLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                         ; SM00410;
; SM00281;
; SM00282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                       IG_like; 5.
LamB; 2.
LamG; 3.
LDLa; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig_c2.
Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDL_recept_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laminin_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12,
12,
17,
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annotation
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Buril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng 2., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Hennandez J.R., Houck J.,
RA Harris N.L., Harvey D., Telliann T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havels D., Telliann T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B. F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B. F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                            Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Kimmel B.E., Rodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Nelson D.R., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wassenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhe Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smi Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287.2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9V4Y0 PRELIMINARY;
Q9V4Y0; Q9V4Y1; Q9V4Y2; (
Q1-MAY-2000 (TrEMBLrel. )
Q1-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20317033; PubMed-10859168;
Bour B.A., Chakravarti M., West J.M.,
"Drosophila SNS, a member of the immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNS PROTEIN.
SNS OR CG2385 OR CG8278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-224; 334-477; 491-1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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AF254867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. 14:1498-1511(2000).
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13, Created)
15, Last sequence update)
17, Last annotation update)
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immunoglobulin su
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                                                                                                                                                                              Yao Q.A.,
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                                                                                           RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Buril J.F., Adbayani A., An H.-J., Andrews-Pfannkor C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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Best Local :
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01-MAY-2000
01-JUN-2001
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CONFLICT
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SEQUENCE
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota;
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AE003835;
AE003835;
AE003835;
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                                                                       . <del>D</del>
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SM00408;
                            M., K.
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IPR003600;
     Lei Y
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Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanogaster (Fruit fly)
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1482
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AAF59042.1;
AAF59043.1;
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AA; 162163
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AAF59038.1;
AAF59039.1;
AAF59040.1;
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Ig_c2.
Ig_like.
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Last sequential Last annotation
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Pred. No.
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E -> EAIWQLEACPSOFAMDLPAPPVHFAGARRFHDNIRF
ACOSLKLRPFFLRTHSYLIPLPCPIRILCPCPPTGTPDMPQ
PT (IN REF. 2).

C -> F (IN REF. 2).

A -> T (IN REF. 2).
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MW; 100C730FA1FA5397
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RESULT
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Best Local
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Q9NBA1;
01-OCT-2000 (TremBLrel. 15,
01-OCT-2000 (TremBLrel. 17,
01-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0033159; Dscam.
InterPro; IPR000267; Aspargnse_glutamnse.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003060; Ig_MHC.
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                                 EMBL; AF260530; AAF71926.1; FlyBase; FBgn0033159; Dscam InterPro; IPR000267; Asparg: InterPro; IPR003961; FN_III
                                                                                                                                                                                                                                                                                                              Dixon J.E., Zipursky S.L.;
"Drosophila Dscam is an Axon Guidance
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20348742; PubMed=10892653; Schmucker D., Clemens J.C., Shu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterigota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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SMART; SM00408;
SMART; SM00410;
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                                                                                                                                                                                                                                               Extraordinary Molecular Diversity. Cell 101:671-684(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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P40189; 1BQU.
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12; Conser
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; IGC; 7.
0; IG_like; 2.
0; IG_Sike; 2.
1144; ASN_GIN_ASE_1; U
J144; ASN_GIN_ASE_1; U
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                                                                                                                                                                                                              TO IMMUNOGLOBULIN
                                 Aspargnse_glutamnse FN_III.
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54.5%;
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Pred. No.
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4; Mismatches
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64A8DE3BB7BD0AB0 CRC64;
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                                              RA Ballew R.M., Basua A., Baxendale J., Buyraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriera S., Fleischmann W.,
RA Choten K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Goorg F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laikh M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
La Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nivon K., Nisekorn D.
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Pfam; PF00047; ig; 10.
SMART; SM00060; FN3; 6.
SMART; SM00408; IGC2; 7.
SMART; SM00410; IG_like; 3.
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Q1-MAY-2000 (TrEMBLrel. 1
Q1-QCT-2000 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
HIBRIS PROTEIN.
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., F Reinert K., Remington K., Saunders R.D.C., Scheeler F., S
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Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00144; ASN_GLN_ASE_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003600; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of 
Submitted (DEC-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QNITARIGEPLVLKCKGAPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 54.1
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG7449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musoa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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222124 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes
to the
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Ig_MHC.
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15,
17,
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e EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (Trew
01-OCT-2000 (Trew
01-JUN-2001 (Trew
W06H8.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spler E., Spradling A.C., Stapleton M., Strong R., Sun E., Syradling A.C., Stapleton M., Strong R., Sun E., Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                         "The sequence of C. Submitted (MAR-1999
                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003812; AAF58172.2
FlyBase; FBgn0029082; hbs.
Interpro; IP8003961; FN_II
Interpro; IP8003598; Ig_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                   Submitted
                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                      Q9N5C2;
                                                                                                                                                                                                                                                                                                                                                                                                  Q9N5C2
  InterPro;
                                                              Waterston
                                                                                                                                   Wilson
                                                                                                                                                                                 investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                    None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003961; FN_III. interPro; IPR003598; Ig_c2. interPro; IPR003600; Ig_like. InterPro; IPR003006; Ig_MHC. pfam; PF00041; fn3; 1.
                                                                                                                                                                                                         'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
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                           DOMAIN.
                                     SIMILARITY:
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              AC006695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00060; FIL.;
SM004108; IGC2; 3.
SM00410; IG_11ke; 6.
SM00410; IG_11ke; 6.
E; PS00290; IG_MHC; UNKNOWN_1.
FILE AA; 132053 MW; 62C0D64968141C9F
                                                                                                                                   ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 37.9
9; Conservative
  IPR003598;
                                     (MAR-2000) to the EMBL/ONTY: TO IMMUNOGLOBULIN
                                                                                                            (MAR-1999)
                                                                                                                                                                                                                                                                                                    Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                  ) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                         Peloderinae;
             AAF39981.1;
                                                                                                                                                                                                                               PubMed=9851916
                                                                                                           elegans) to the
Ig_c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.8%;
                                                                                                                                                                                                                                                                                                                                                  15,
15,
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                                                                                                                                                                                          natode C. elegans: a pl
C. elegans Sequencing
                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                EMBL/GenBank/DDBJ databases
                                                                                                           cosmid W06H8.";
EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.1
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                      AND
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                                     MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                    Rhabditida; Rhabditoidea;
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                                     HISTOCOMPATIBILITY
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                                                                                                            databases
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                                                                                                                                                                                           platform for
ng Consortium.";
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InterPro; IPR003006;
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2;
SMART; SM00410; IG_1i
SEQUENCE 1791 AA;
                                              InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                    EMBL;
                                                                                                                                                            Mitchell M.S., Kan-Mitchell J., Minev B., "Identification of a novel melanoma gene IL-1 receptor antagonist - which encodes cytolytic T lymphocytes.";
Submitted (OCT-1999) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                    Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y
Tanaka A., Kotani H., Miyajima N., Nomura N.;
"Prediction of the coding sequences of unidentified human
The coding sequences of 80 new genes (KIAA0201-KIAA0280)
analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1708
                           InterPro;
InterPro;
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InterPro;
                                                                                                            HSSP;
                                                                                                                                                                                                               TISSUE-MELANOMA;
                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                             Genomics
                                                                                                                                                                                                                                                      chromosome 2p25
                                                                                                                                                                                                                                                                                            TISSUE=MELANOMA;
MEDLINE=95048383;
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BONE MARROW;
MEDLINE=97191544; PubMed=9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q92626;
                                                                                                                                                                                                                                                                                    Weiler S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYELOBLAST KIAA0230 (FRAGMENT).
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                                                                                                                                                                                                                                                                          Trent J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                "Assignment of a human melanoma
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                                                                                                          P05164; 1CXP
                                                                                                                     D86983; BAA13219.1; AF200348; AAF06354.
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13; Conser
                 ; IPR003006;
; IPR001611;
; IPR000483;
; IPR000372;
; IPR003591;
; IPR001536;
; IPR002016;
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.R., Taylor S.M., Deans R
                                                                                                                                                                                                                                             22:243-244(1994).
         IPR001007;
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7 (TrEMBLrel. 02, I
1 (TrEMBLrel. 17, I
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IG_like; 3.
AA; 199071 MW;
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                                              Ig_MHC.
LRR.
LRR_Cterm.
LRR_Nterm.
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Ig_MHC.
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48.1%;
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Ig_c2.
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Pred. No.
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Catarrhini;
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                                                                                                                                                                              C., Deans R.J.;
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s recognized by
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Matches 11
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SMART; SM00408; IGc2; 4.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRR TYP; 4.
SMART; SM00014; VWC; 1.
                                                                                  PRINTS; PRO0109; TYRKINASE.

SMART; SM00410; IG_like; 3.

SMART; SM00410; IG_like; 3.

SMART; SM00219; TYTKC; 1.

SMART; SM00219; TYTKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

ATP-binding; Transferase; D0A52ED6A8760C07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
Pfam;
                                                                                                                                                                                                                                                                                  Miller M.A., Steele R.E.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                             Q25198
Q25198;
                                                                                                                                                                          Pfam; PF00047; ig; 5. Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                              EMBL; U59448; AAB03389.1; -. HSSP; P06213; 1IRK.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metaz
Hydridae; Hydra.
NCBI_TaxID=6087;
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RECEPTOR TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                            Hydra attenuata (Hydra) (Hydra
Eukaryota; Metazoa; Cnidaria; H
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                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                    [nterPro;
                                                                                                                                                                                                                            InterPro;
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            Ν
                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNITARIGEPLVLKCKGAPKKPPQRLEW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00141;
PF00093;
KNITAYIGEPAWVHCQGKGFPK
                                      l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 39.3
11; Conservative
                                                                                                                                                                                          | IPR003598; Ig_c2.
| IPR003600; Ig_like.
| IPR003006; Ig_MHC.
| IPR001245; Tyr_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01208; VWFC; UNKNOWN_1.
                                                                                                                                                                                                                                   IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1496 AA;
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                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxidase;
vwc; 1.
                                                                                                                                                                                                                                                                           IMMUNOGLOBULIN
                                              34.0%;
59.1%;
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17,
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                                     2;
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                                              Score
Pred.
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Pred.
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Hydrozoa; Hydroida;
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                                      Mismatches
                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
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                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                         848
                                                                                                                                                                                                                                                                          MAJOR HISTOCOMPATIBILITY COMPLEX
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                                     5.
                                                        Length 848
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                                                                                                                                                                                                                                                                                                                                            Anthomedusae;
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                                    2;
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                                    Gaps
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Query Match
Best Local S
Matches 10
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD: MGI:1343102; Rbig1.
InterPro: IPR003961; FN_III.
InterPro: IPR003598; Ig_c2.
InterPro: IPR003006; Ig_MHC.
Pfam; PF00041; fn3; 3.
Pfam; PF00047; ig; 5.
SMART; SM0060; EN3; 3.
                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Z2I4
Q9Z2I4;
                                                                              EMBL; AL117666; CAB56036.1; ... Interpro; IPR003598; Ig_c2. Interpro; IPR003006; Ig_MHC. pfam; pr00047; Ig; 2. SMART; SM00408; IGc2; 2.
                                                                                                                                        Duesterhoeft A., Lauber J.,
Submitted (SEP-1999) to the
-!- SIMILARITY: TO IMMUNOGLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00060;
SMART; SM00408;
SEQUENCE 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                  Hypothetical protein.
NON_TER 1
SEQUENCE 483 AA; 5
                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Yuan S.-S.F., Cox L.A., Submitted (APR-1998) to -!- SIMILARITY: TO IMMUN
                                                                                                                                                                                                                                                                                                               Q9UF14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                           TISSUE-UTERUS;
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  DKFZP58601624.
                                                                                                                                                                                                                                                           HYPOTHETICAL 51.9
                                                                                                                                                                                                                                                                                                    Q9UFI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1343102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                NVVVAVGEPAVMECVPPKGHPEPLVTWK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P56276;
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
           Similarity
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                          KDA PROTEIN (FRAGMENT).
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Rodentia;
                                                                                                                                             IMMUNOGLOBULIN
                                                                                                                                                                                                                  Chordata;
Primates;
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                                                    51907
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32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dasika G.K., Lee E.Y.-H.P.;
the EMBL/GenBank/DDBJ databases.
NOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                    ₩;
                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 54; DB; Pred. No. 22; 5; Mismatches
                                                                                                                                           Mewes H.W., G
EMBL/GenBank/
OBULIN AND MAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
Score 53.5; DE Pred. No. 9.2; 4; Mismatches
                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                   B3DFEC945C0DF8FC
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                                                                                                                                                                                                                                                                                                               483
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22;
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                    Length 483;
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Title:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                             00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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AAY 52135
AAW 44208
AAW 33762
AAW 44214
AAW 33768
                                             AAY09349
AAY52134
                AAW44200
AAW33754
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RAGE
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soluble RAGE
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Mouse RAGE V-dom Rat RAGE V-dom Rat RAGE V-dom Rat RAGE V-do N-terminal sequ Harabidopsis tha Arabidopsis tha Haemophilus influman V-domain Peptide #3823 e Arabidopsis tha Zea mays protei Zea mays protei Human secreted Human secreted Human secreted Human secreted Arabidopsis tha Human secreted Arabidopsis tha Human secreted Arabidopsis tha Human secreted Arabidopsis tha Human secreted Xea mays protei Zea mays protei	Human soluble Human RAGE pol Extracorporeal
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## ALIGNMENTS

AAY09353 RESULT

AAY09353 standard;

peptide;

10 AA

AAY09353;

09-JUL-1999 (first entry)

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RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; senility; renal failure; hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral scherosis; multiple scherosis; amyloidosis; autoimmune disease; inflammation; testing the scherosis; amyloidosis; autoimmune disease; inflammation;
          WPI; 1999-277439/23
                                                                                 09-OCT-1997;
                                                                                                          09-OCT-1998;
                                 Lamster I,
                                                         (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                  22-APR-1999
                                                                                                                                                        WO9918987-A1
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                       neuropathy;
                                                                                                                                                                                                                                                                                                     Human RAGE V-domain peptide SEQ ID NO:5.
                                                                                                                                                                                                                    cancer;
                                 Schmidt AM,
                                                                                                                                                                                                       retinopathy;
                                                                                 97US-0948131.
                                                                                                          98WO-US21346
                                                                                                                                                                                                                    male impotence; wound
                                 Stern D,
                                                                                                                                                                                                       nephropathy;
                                 Yan
                                                                                                                                                                                                                    healing;
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                                 SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's disease, sentlity, renal failure, hyperlipidaemic atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia associated with head trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis, an autoimmune disease, inflammation, a tumour, cancer, male impotence, wound healing, periodontal disease, neuropathy, retinopathy, nephropathy or neuronal degeneration.
WPI; 2000-013260/01
                                                                                                                                                                                                                                                                                   Soluble receptor for advanced glycation endproducts; RAGE; tumour; invasion; metastasis; amphoterin; neuron; inhibit; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes novel isolated peptides (I) amino acid sequence corresponding to an amino acid sequence
                                   Schmidt AM,
                                                                                                         17-APR-1998;
                                                                                                                                                                             28-OCT-1999
                                                                                                                                                                                                              W09954485-A1
                                                                                                                                                                                                                                                                                                                                        Human Receptor to
                                                                                                                                                                                                                                                                                                                                                                                                               AAY52135;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY52135 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides based on an advanced glycation end product receptor are useful for treating Alzheimer's disease and Down's syndrome
                                                                    (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                            16-APR-1999;
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The present sequence represents an immunologically active fragment of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes
                                                                                         Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts was a range of physiologically and pathophysiologically relevant ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective
                                                            Claim 2; Page 46; 90pp; English
                                                                                                                                                        WPI; 1997-558580/51
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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AGE; antibody; vascular permeability; immunologically active
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                                                                                                                                                                                                                   (SCHD ) SCHERING PATENTE AG.
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                                                                                                                                                                                This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active fragments or their mimetics can inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly compilications such as micro- or macro- vasculopathy or occlusive vascular
                 disorders such as neuropathy, nephropathy, atherosclerosis or retinopathy) or haemodialysis-associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or age-related disorders such as oxidative stress. These RACE polypeptides are also used, when immobilised, to purify AGE from a protein mixture are some for compounds that are agonists and antagonists of AGE/RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
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can also be used
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diabetes mellitus; treatment; atheroscleros
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Best Local
                                                          of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vasculated amyloidosis or atheroselerosis. The Ab can also be used for the contraction and the contraction between the contraction between the contraction of the contraction between the contraction of the contraction between the contraction between the contraction between the contraction of the contraction between the contrac
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                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Advanced glycosylation end-product receptor; RAGE; screening; AGE; vascular permeability; diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                                                                                                                   genes
                                                                                                                                                                                                                                                     interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-526458/48
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                                                                                                                                                                                                   CC (ABP) interaction with a receptor for RAGE when the receptor is on the control of a cell; (2) inhibiting degeneration of a neuronal cell; (3) CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting CC extracellular assembly of an ABP fibril on a cell; (6) inhibiting CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration CC of a microglial cell into senile plaques; (7) inhibiting activation of a CC microglial cell by an ABP; (8) treating a subject with a condition CC associated with an interaction of an ABP with a receptor for RAGE on a CC cell; (9) evaluating the ability of an agent to inhibit binding of an CC ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10) CC inhibiting activation of an SW kappas gene in a cell; (11) inhibiting CC inhibiting activation of an CK kappas gene in a cell; (11) inhibiting CC inhibiting activation of a subject; (12) inhibiting an RAGE's interaction CC with a receptor for RAGE when the receptor is on the surface of a cell; CC and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods CC can be used for treating conditions associated with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell. Schalmer's conditions associated with an interaction of an CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzhelmer's conditions associated with an interaction of an CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzhelmer's conditions associated with a condition condition condition conditions associated with a condition condit
                                                                                                                             disease, senility, renal failure, hyperlipidaemic atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia associated with head trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence corresponding to an amino acid sequence of a V-domain of a receptor for an advanced glycation end product (RAGE). V-domain of a receptor for an advanced glycation end product (RAGE). Also described are methods for: (1) inhibiting an amyloid-beta peptide (ARA) interaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                       an autoimmune disease, inflammation, a tumour, cancer, male impotence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes novel isolated peptides (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides based on an advanced glycation useful for treating Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-277439/23
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                                                                           periodontal disease, neuropathy, retinopathy, nephropathy
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                                                                                                                                   amyloidosis,
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                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RACE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
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                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting tumour invasion or spreading by administration of receptor for advanced glycation endproducts -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGE (RAGE) amino acid sequence fragment #3
                                                                                                                   0;
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Pred. No. 0.0
); Mismatches
                                                                                                                                              Score 10;
Pred. No.
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                                                                                                                   Mismatches
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0.00027;
                                                                                                                                              DB 21;
0.00027;
                                                                                                                   0;
                                                                                                                                                                          Length 30;
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                                                                                                                Gaps
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RESULT

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                                                                                                AAW33754
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                                                                                                                RESULT
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                      glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AAE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.
Human RAGE polypeptide (318 amino acid residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mature receptor to an advanced glycosylation end product.
                             08-MAY-1998
                                                         AAW33754;
                                                                                   AAW33754 standard;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a mature human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 42-43; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hollander DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCHD ) SCHERING PATENTE AG.
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                                                                                                               10
                                                                                                                                                       1 aqnitarige 10
                                                                                                                                                                                 1 AQNITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody;
                                                                                                                                                                                                                                                                                     318
                                                                                                                                                                                                              Conservative
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                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; advanced glycosylation end product; RAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascular permeability; diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0633148
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                                                                                     Protein;
                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                     318
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                            Score 10;
Pred. No.
                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                          DB 18;
0.0019;
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RESÜLT 1
AAY52130
ID AAY5
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular disorders such as neuropathy, nephropathy, retinopathy or atherosclerosis) or haemodialysis associated amyloidosis, also activation of microglial cells by beta amyloid peptides in Alzheimer's disease or age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (318 amino acid residues). The RAGE polypeptides and its active fragments or their mimetics, inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
Soluble receptor for advanced glycation endproducts; RAGE; invasion; metastasis; amphoterin; neuron; inhibit; therapy
                                                                                 28-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                            interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Advanced glycosylation vascular permeability; Alzheimer's disease.
                                               Human Receptor to AGE (RAGE) amino acid sequence
                                                                                                                  AAY52130,
                                                                                                                                               AAY52130 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                genes.
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                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                1 AQNITARIGE 10
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DB; AAV06518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Fig 1B; 91pp;
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                               318
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                                                                                                                                                                                                                                                                                               Conservative
                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end-product receptor; RAGE; screening; AGE;
diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                                332 AA
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                           DB 18;
0.0019;
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                                                                                                                                                                                                                                                                                                                            Length
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                 RAGE; tumour;
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AAW44199
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                               both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the human soluble Receptor Advanced Glycation Endproducts (RAGE). RAGE interacts with a rphysiologically and pathophysiologically relevant ligands when
          16-APR-1996;
                                   11-APR-1997;
                                                            23-OCT-1997
                                                                                     WO9739125-A1
                                                                                                             Homo sapiens
                                                                                                                                                                          Human soluble
                                                                                                                                                                                                   14-MAY-1998
                                                                                                                                                                                                                           AAW44199
                                                                                                                                                                                                                                                   AAW44199 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 10-11; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO )
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                                                                                                                                                                                                                                                                                                                            1 AQNITARIGE
                                                                                                                                                                                                                                                                                                               1 aqnitarige 10
                                                                                                                                      antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 advanced glycation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA
                                                                                                                                                                          receptor to an advanced
                                                                                                                                      vascular permeability; diabetes mellitus
                                                                                                                                                 receptor; advanced glycosylation end product; RAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0062365
           96US-0633148
                                    97WO-EP01834
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                                                                                                                                                                                                                                                   Protein; 340
                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No.
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                                                                                                                                                                         glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                          end product.
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RESULT 1
AAW33753
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevents receptor permeability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
         New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabete etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                   WO9739121-A1
                                                                                                                                                                                                                                                                                     Alzheimer's disease
                                                                                                                                                                                                                                                                                                Advanced glycosylation vascular permeability;
                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33753 standard; Protein; 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                  Morser MJ,
                                                                                                                                                      16-APR-1996;
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                                                                                                                                                                                                                                                             Homo
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                                                              N-PSDB;
                                                                                                                            (SCHD ) SCHERING AG
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                                                            1997-526458/48
DB; AAV06517.
                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                      RAGE polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 AA;
                                                                                                  Nagashima
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                                                                                                                                                      96US-0633147
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                                                                                                                                                                                                                                                                                                end-product receptor; RAGE;
diabetes mellitus; treatment
                                                                                                                                                                                                                                                                                                                                      (340 amino acid residues).
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0.002;
                                                                                                                                                                                                                                                                                                treatment; atherosclerosis;
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                                                                                                                                                                                                                                                                                                            screening; AGE;
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                                                                                     Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           active fragments or their mimetics, inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). The are used to treat diseases associated with AGE/RAGE interaction, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (340 amino acid residues). The RAGE polypeptides and i active fragments or their mimetics, inhibit interaction between ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB81925
                                             Claim 1; Page 31-32;
                                                                         dysfunction
                                                                                                                                                                                                               (TORA )
                                                                                                                                                                                                                                               08-SEP-1999;
                                                                                                                                                                                                                                                                              08-SEP-2000; 2000WO-JP06172
                                                                                                                                                                                                                                                                                                            15-MAR-2001
                                                                                                                                                                                                                                                                                                                                       WO200118060-A1
                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                      diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                   Extracorporeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracorporeal circulation material receptor protein
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10; Conserv
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                                                                                                                                                                                                                  TORAY IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 404
                                                                                                                                                                                                                                                                                                                                                                                                      vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                   circulation;
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                                                                           lesions
                                           Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                   carbonyl stress product; receptor;
excretory dysfunction.
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The present invention describes a material for extracorporeal which is made from a water-insoluble carrier immobilized with

circulation a protein

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CC amino acid sequence corresponding to an amino acid sequence of a CC V-domain of a receptor for an advanced glycation end product (RAGE). CC Also described are methods for: (1) inhibiting an amyloid-beta peptide CC (ABP) interaction with a receptor for RAGE when the receptor is on the Surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) cC inhibiting formation of an ABP fibril on a cell; (4) inhibiting CC extracellular assembly of an ABP into a fibril; (5) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a microglial cell into senile plaques; (7) inhibiting activation of a ssociated with an interaction of an ABP with a receptor for RAGE on a CC cell; (9) evaluating the ability of an agent to inhibit binding of an CC inhibiting activation of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a RAF with a v-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a RAF with a v-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAGE; V-domain; receptor for advanced glycation endproduct; ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; senility; renal failure; hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation; multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        having the sequence shown here. The materials of the invention, including adsorbents, are for extracorporeal circulation, which are applicable in the selective elimination of diabetic complication factors from a body fluid, and are therefore useful in treating vascular lesions like arteriosclerosis due to carbonyl stress products caused by abnormally promoted carbonyl stress from excretory dysfunction.
                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                           New peptides based on an advanced glycation end product receptor are useful for treating Alzheimer's disease and Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCO ) UNIV COLUMBIA NEW YORK.
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male impotence; wound healing; periodontal disease;
inopathy; nephropathy; neuronal degeneration.
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                                                                                                                                    periodontal disease in a subject; (12) inhibiting an RAGE's interaction with a receptor for RAGE when the receptor is on the surface of a cell; and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE, e.g. diabetes, Alzhelmer's disease, senility, renal failure, hyperlipidaemic atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia associated with head trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis, an autoimmune disease, inflammation, a tumour, cancer, male impotence, wound healing, periodontal disease, neuropathy, retinopathy, nephropathy or neuronal degeneration.
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Search completed: April 24, 2002, 09:21:51 Job time: 250 sec

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Copyright (c) 1993 - 2000 Compugen
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US-08-477-358-191
US-09-188-930-153
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US-08-420-526-11
US-08-427-238-11
US-08-427-238-11
US-08-427-173-16
US-08-487-167-16
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US-08-487-167-16
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US-08-615-271-16
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Sequence 191, App
Sequence 113, App
Sequence 115, App
Sequence 115, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 16, Appl
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	Sequence 6, Appli	Sequence 68, Appl	Sequence 68, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 24, Appl	Sequence 10, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 36, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 11, Appl	Sequence 7, Appli

ALLGNMENTS

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 326-2400
; MOLECULE TYPE: peptide US-08-633-148-12
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES ANI
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRIET: TWO EMBARCADERO CENTER, 8TH FLOOR CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A
ZIP.
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                    TYPE: amino acid
STRANDEDNESS: sir
                                     TOPOLOGY:
                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08633148
                                                                                            15 amino acids
                                 ss: single
linear
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                         08-633-148-4
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                  squence 4, Application US/08633148 stent No. 5864018
                                                                                                        APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO.
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND
                                                                                                                                                                                                                ENERAL INFORMATION:
                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
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ADDRESSE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
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TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
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                                                                                             NUMBER OF SEQUENCES:
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                  SAN FRANCISCO
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CALIFORNIA
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HOLLANDER, DORIS A.
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Pred. No.
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                                                                                                                RECEPTOR POLYPEPTIDES AND USES THEREFOR
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                               FILING DALL.

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REGISTRATION NUMBER: 014618

TELECOMMUNICATION INFORMATION:

TOTAL POHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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Best Local Similarity
TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0)
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 16-APF
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HOLLANDER, DORIS A.
                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                             014618-005600US
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Pred. No. 0.00038;
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                                                                 RESULT 6
US-08-473-750-7
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Sequence 7, Application US/08473750 Patent No. 5834187
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Best Local Similarity 100.0%;
Matches 10; Conservative (
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Best Local
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APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charles C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,231A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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LENGTH: 741 amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                              157 TARIGE 162
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TOPOLOGY: linear
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ZIP: 02173
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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Two Militia Drive
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100.0%;
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Pred. No. 0.0004;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                        US-08-477-326-7
                                                                                                                                                                       APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
Patent No. 5568769
                                                                                                                                                                                                                                                                    Sequence 7, Application US/08477326 Patent No. 5968769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles
TITLE OF INVENTION: Sequence and
Patent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: CATTOL1, ALICE O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Structural Gene and the LKP TITLE OF INVENTION: Haemophilus Influenzae NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: Hamilton, Brook, Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 741 amino acid
TYPE: amino acid
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APPLICATION NUMBER: US 08/277,321
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MEDIUM TYPE: Floppy disk
                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                 APPLICANT: Green, Bruce A. APPLICANT: Brinton, Jr., Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   157 TARIGE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
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COUNTRY: UZIP: 02173
                                 STATE: Massachusetts
                                                                   STREET:
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                                                  Lexington
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                                                              E: Hamilton, Brook, Smith & Reynolds,
Two Militia Drive
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and Analysis of LKP Pilin
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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Best Local :
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ATTORNEY_AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)_873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-637-759B-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                      FILING DALE.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB95/02875
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
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FILING DATE: July 19, 199
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
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STREET: 1201 W
CITY: Atlanta
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
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les 6; Conserv
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                                                                                                                                                                                                                         APPLICATION NUMBER:
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100.0%; Pr
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c; Pred. No. 18;
d; Mismatches
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5. 18;
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Query Match
Best Local Similarity
"~+~hes 5; Conserv?
                                                                                                               ; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-871-355A-191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6015669
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                 TELEFAX: (404) 873-8795 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB95/02875
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Stre
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/CFILING DATE: 11-DEC-1995
CLASSIFICATION: 435
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TYPE: amino acid
STRANDEDNESS: single
2 QNITA 6
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                        STRANDEDNESS:
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ZIP: 30309-3450
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STATE: Georgi
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                                           Conservative
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Pred. No.
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RESULT 10 US-09-188-930-153

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US-08-43-238-11
US-08-43-238-11
; Sequence 11, Application US/08543238
; Patent No. 5607919
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US-09-188-930-304
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Best Local S
Matches 5
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 153
LENGTH: 72
TYPE: PRT
                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 304 LENGTH: 72 TYPE: PRT
                                                                                                                                                                                           Matches
                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 304, Application US/09188930A Patent No. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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47 ARIGE 51
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                                                                                                                                                                                                           50.0%;
100.0%;
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100.0%; Pred. No
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Mismatches
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Query Match
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION UNMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Bojsen,
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                                                                                                                                                                                                         APPLICANT: Bojsen, Kirsum.
APPLICANT: Kragh, Karsten M.
APPLICANT: Mikkelsen, Jorn D.
APPLICANT: Nielsen, Klaus K.
TTTLE OF INVENTION: Anti-Microbial Proteins
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc.
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT: Nielsen, Klaus K.
TITLE OF INVENTION: Anti-Microbial Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                 STREET: 975 Cal:
CITY: Palo Alto
STATE: CA
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ZIP: 94304
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975 California Avenue
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415/857-1125
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US/08/420,526
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Pred. No.
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o. 56;
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FILING DATE: CLASSIFICATION:

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Best Local :
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                                                                TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                               NAME: Stewart, Michael I REGISTION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                               APPLICATION NUMBER: US/08
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Analog of Haemophilus Hing
TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415/354-3588
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NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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LENGTH: 146 amino acid
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               STRANDEDNESS:
TOPOLOGY:
                                              LENGTH:
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м5G 1R7
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                             amino acid
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Suite 701, 330 University Avenue
                                              198 amino acids
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CHONG, Pele
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linear
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Pred. No.
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o. 56;
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Query Match

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Score 5;

DB 1;

Length 198;

Search completed: April 24, 2002, 09:22:30 Job time: 249 sec

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US-08-483-859-16
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                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHONG, PEAPPLICANT: COMEN, RAPPLICANT: KLEIN, MAPPLICANT: KLEIN, MITTLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                FILING DATE: 21-JUL-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                       NAME: Stewart, Michael: REGISTRATION NUMBER: 24. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
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43 TARIG
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VENTION: Analog of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                               (416)
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                                                       Conservative
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595-1163
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

protein search, using sw model

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9 April 24, 2002, 09:23:17; Search time (without alignments)
19.709 Million cell updates/sec 38.65 Seconds

Perfect score: Title:

1 AQNITARIGE 10

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size :

Total number of hits satisfying chosen parameters: 219241

Minimum Maximum DB DB seq length: 0 length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR\_68:\*

and is score Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, a derived by analysis of the total score distribution.

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10		8	7	6	ر ت	4	ω	2	_	Result
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hypothetical prote	hypothetical prote	barwin homolog whe	hypothetical prote	barwin homolog whe	pathogenesis-relat	acyl carrier prote	.conserved hypothet	barwin - barley	0	_	thetical p	p24 protein - born	outer membrane ush	recombination prot	threoninetRNA li	_		hypothetical prote	argininosuccinate	hypothetical prote	probable integrase	RNA helicase RH17		membrane antigen g	₹		probable advanced	advanced glycosyla	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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N	N	2	Ν	Ν	N	N	N	2	2	N	Ν	N	ν	2	Ν
T51827	S30165	G70874	A83092	C72071	E86553	T09136	T50361	S20593	T10192	S75124	JN0681	A82946	S38089	H64329	S67038
MADS-box Protein [	repressor protein	probable transcrip	probable phosphohe	DNA-3-methyladenin	3-methyladenine DN	ADP-ribosylation f	hypothetical prote	alcohol dehydrogen	senescence-associa	thioredoxin-like p	gamma2-crystallin	ribosomal protein	hypothetical prote	hypothetical prote	ribosomal protein

### ALIGNMENTS

advanced glycosylation end-products receptor precursor - human N.Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot

C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999
C:Accession: I61596; B42879; S27968
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, Genomics 23, 408-419, 1994
A;Title: Three genes in the human MHC class III region near the junction with the cla

nterpart of mouse mammary tumor gene int-3. A; Reference number: A55562; MUID:95137587

A; Accession: I61596

A; Status: nucleic acid sequence not shown; translation not shown; translated GB/

A; Molecule type: DNA A; Residues: 1-404 < RES>

A;Cross-references: GB:D28769; NID:9561657; PIDN:BAA05958.1; PID:9561659
R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston,

R:Neeper, M.; Schmidt, A.M.; Brett, J.; Ya J. Biol. Chem. 267, 14998-15004, 1992 A:Title: Cloning and expression of a cell A;Reference number: A42879; MUID:92340547 A:Accession: B42879 surface receptor for advanced glycosylation

A;Molecule type: mRNA A;Residues: 'G',2-99,'R',101-404 <NEE> A;Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846

A; Experimental source: lung
A; Note: sequence extracted from NCBI backbone (NCBIP:109438)

C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Genetics:

A;Gene: GDB:AGER
A;Cross-references: GDB:306354; OMIM:600214
A;Map position: 6p21.3-6p21.3
A;Map position: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2
A:Tntrons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2 neuronal receptor for amphoterin, a DNA-binding protein involved in ne

A,Description: neuronal receptor for amphoterin, a DNA-binding process in the control of the con

receptor #status predicted <MAT

F;23-344/Domain: extracellular #status predicted <EXT>
F;31-101/Domain: immunoglobulin homology <IM1>

F;137-210/Domain: immunoglobulin homology <IM2>F;252-303/Domain: immunoglobulin homology <IM3>

F;363-404/Domain: transmembrane #status predicted <TMM>
F;363-404/Domain: intracellular #status predicted <INT>
F;25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted F;38-99,144-208,259-301/Disulfide bonds: #status predicted

ne

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probable advanced glycosylation end-products receptor precursor - mouse k; Alternate names: RAGE C; Species: Mus musculus (house mouse) C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000 C; Date: 11-Jun-1999 #sequence 21-Jan-2000 C; Date: 11-Jun-1999 #sequence 21-Jan-2000 C; Date: 11-Jun-1999 #sequence 21-Jan-2000 R; R; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Losubmitted to the EMBL Data Library, October 1997 R; Description: Sequence of the mouse major histocompatibility locus class I:
                       A; Molecule type: protein
A; Residues: 23-24, 'x', 26-37, 'x', 39-49, 'xx', 52-54 <SCH>
A; Residues: 23-24, 'x', 26-37, 'x', 39-49, 'xx', 52-54 <SCH>
A; Reperimental source: endothelial cells
A; Note: sequence extracted from NCBI backbone (NCBIP:109434)
C; Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosylation, thus contributing to tissue lesions in diabetes.
                                                                                                                                                                                                                                A;Cross references: GB:M91212; NID:g163650; PIDN:AAA03575.1; PID:g163651
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein,
A;Note: parts of this sequence, including the amino end of the mature protein,
A;Note: ham.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposit
J; Biol. Chem. 267, 14987-14997, 1992
A;Fitle: Isolation and characterization of two binding proteins for advanced g.
A;Reference number: A42878; MUID:92340546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           advanced glycosylation end-products receptor precursor - bovine
Nalternate names: advanced glycosylation end product-binding protein, 35K; glycoprote
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: A42879; A42878; S27949
R;Neeper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation
A;Reference number: A42879; MUID:92340547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1;
C:Superfamily: advanced glycosylation end products
C:Keywords: receptor; transmembrane protein
E:31-100/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-416 <NEE>
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A; Residues: 1-402 < R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T09062
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                                                                                                                                                                                                              A; Accession: A42878
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9; Consert
        receptor appears also
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Pred. No. 0.0005;
Mismatches 0
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        6
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     amyloid beta peptide on
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                                                                                      R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI A;Reference number: A93065; MUID:85035713
A;Accession: F43044
                                                                                                                                                                                                                                membrane antigen gp85 - human herpesvirus 4 (strain B95-8) C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_c C;Accession: F43044; A03787; S33040
                                                                                                                                                                                                                                                                                                                                                          RESULT
QQBE43
A;Molecule type: DNA
A;Residues: 1-234 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24835.1; PID:g1334899
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F;31-100/Domain: immunoglobulin homology <IM1>
F;136-209/Domain: immunoglobulin homology <IM2>
F;236-313/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: transmembrane #status predicted f;373-416/Domain: intracellular #status predicted F;275,80/Binding site: carbohydrate (Asn) (covalent F;25,80/Binding site: carbohydrate (Asn) (covalent F;38-98,143-207,269-311/Disulfide bonds: #status p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ates in the neurotoxic pathway that produces dementia in Alzheimer's disease. C;Function:
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homo C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F;23-354/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                       A;Gene: mutH
C;Superfamily: mutator mutH
                                                                                                                                                                                                                                                                                                                                                                                    A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, A; Title: Whole-genome random sequencing and assembly of Haemophilus influence number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ker; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; V., D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: DNA mismatch protein C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision
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A; Residues: 1-223 <TIGR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutator mutH - Haemophilus influenzae (strain
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밁
                                                                                                                                                                                                                                                                         A; Cross-references: GB:U32723;
                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
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Best Local
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165 ITARIGE
                                                                                        Local Similarity
nes 7; Conserv
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                                          4 ITARIGE 10
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Pred. No.
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И.; Weidman
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Barrell, B.G.

#text\_change

16-Jul-1999

fragment C

of

B95-8

Epstein-Barr

24 09:48:12

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RNA helicase RH17 [imported] - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_chang C;Accession: T51746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; A;Title: Whole-genome random sequencing and assembly A;Reference number: A64000; MUID:95350630
A;Accession: H64181
A;Status: nucleic acid sequence not shown; translatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID: 84270667
A;Contents: annotation; protein coding region C;Superfamily: Epstein-Barr virus membrane antigen gp85
ρ
                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T51746
                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 27, 628-636, 1999
A; Title: The DEAD box RNA helicase family
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Nature 310,
                                                                                                                                                                                    A;Cross-references: EMBL:AJ010468; PIDN:CAA09207.1
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-298 < AUB>
                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                  R; Aubourg, S.; Kreis, M.; Lecharny, Nucleic Acids Res. 27, 628-636, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L42023; TIGR:HI1079 C;Superfamily: histidine permease protein I
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A; Residues: 1-238 <TIGR>
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Pred. No.
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                                    Indels
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RESULT
H69133
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A;Title: Molecular analysis of a cytotoxin-converting phage, A;Reference number: S33665; MUID:93225809
A;Accession: S33667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable integrase - Pseudomonas aeruginosa phage CTX
c;Species: Pseudomonas aeruginosa phage CTX
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: S33667
                                           R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicacire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan; ki, S.; Church, G.M.; Dankels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                   argininosuccinate lyase - Methanobacterium thermoautotrophicum (strain Delta C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein R06F6.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #tC;Accession: T23984
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A; Cross-references: EMBL:D13409; NID:g217776; PIDN:BAA02675.1; C; Superfamily: hypothetical protein b1579
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A; Reference number: A69000; MUID:98037514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: Z19826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 68/3; 189/2;
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                                                                                                                                   C; Accession: H69133
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A; Residues: 1-429 <WIL>
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R;Beyan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; I
submitted to the Protein Sequence Database, Februar;
A;Reference number: 215420
A;Accession: T05671
A;Molecule type: DNA
A;Residues: 1-548 <BEV>
A;Cross-references: EMBL:AL035539
A;Experimental source: cultivar Columbia; BAC clone
C;Genetics:
A;Map position: 4
A;Introns: 90/1; 129/1; 302/3; 420/3
A;Note: F22113.200
C;Superfamily: Arabidopsis thaliana hypothetical pro
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                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F22I13.200 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change C;Accession: T05671
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Residues: 1-468 </Th>
A;Residues: 1-468 </Th>
A;Cross-references: GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84775.1; PID:g26213
A;Experimental source: strain Delta H
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A; Molecule type: DNA
A; Residues: 1-471 <NOE>
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A;Description: Distribution and characterization of plasmid-related sequence
A;Reference number: S30583
A;Accession: S30585
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A; Gene: MTH269
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b; Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                    M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, Database, February 1999
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A:Note: belongs to class-II synthetases
C:Superfamily: threonine--tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; l
                                                                                                                                                                                                                                                            A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14684.1; PID:g386
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: thrS; RP221
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A; Residues: 1-635 < AND>
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A;Accession: E71733
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: E71733
C;Accession: E71733
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              threonine--tRNA ligase (EC 6.1.1.3) - Ricke
N,Alternate names: threonyl-tRNA synthetase
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A; Residues: 1-609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402, 761-768, 1999
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recombination protein rec2 - Haemophilus influenzae (strain Rd KW20)
c;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
c;Accession: 164045
R;FLeischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Cocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Itle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Itle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
A;Recession: I64045
A;Retaus: nucleit acid sequence not shown; translation not shown
A;Residues: 1-788 <TICRD
A;Cross-references: GB:U32691; GB:L42023; NID:g1573004; PIDN:AAC21739.1; PID:g1573009; T.C.; Cenetics:
A;Genetics: A;Genetics: GB:U32691; GB:L42023; NID:g1573004; PIDN:AAC21739.1; PID:g1573009; T.C.; Competical Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 76 AQNITA 81
Search completed: April 24, 2002, 09:23:17
Job time: 246 sec
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AMPM_CHLPN	CRTE_RHOSH	LPXA_RICRI	FLGG_AGRTU	DHBA_BACSU	RRPP_ORSVW	RRPP_HRSVL	RRPP_HRSVA	RRPP_HRSV1	RRPP_HRSV	RRPP_BRSVA	MXIJ_SHISO
Q9z6q0 chlamydia p		P32199 rickettsia		P39071 bacillus su	Q83956 ovine respi	P12579 human respi			P14156 human respi		Q55288 shigella so

## ALIGNMENTS

RA R	R R R R R R R R R R R R R R R R R R R	•	R R R R R R R R R R R R R R R R R R R	SU.
SEQUENCE FROM N.A. (ISOFORM 2).  Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,  Schuler A., Huber G.;  "CDNA cloning of a novel secreted isoform of the human Receptor for  "CDNA cloning of a novel secreted isoform of the human Receptor for  Advanced Glycation End products (RAGE) and characterization of cells  co-expressing cell-surface scavenger receptors and Swedish mutant  amyloid precursor protein.";  Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  [6]	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  Banta A., Spies T., Hood L.;  Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.  [4]  SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.  Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,  Yamamoto H.;  "Molecular heterogeneity of the receptor for advanced glycation endproducts.";  Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  [5]	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  MEDLINE-95137587; PubMed=7835890;  Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  Inoko H., Itemura T.;  "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; Genomics 23:408-419(1994).	SEQUENCE FROM N.A. (ISOFORM 1). TISSUE=Lung; MEDLINE=92340547; PubMed=1378843; Meeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C., Elliston K., Stern D., Shaw A.; "Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins."; J. Biol. Chem. 267:14998-15004(1992).	

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

1. FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATED PROTEINS
PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
RATE IN DIABETES.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
BECRETED (ISOFORM 2).

1. ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/RAGESEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hudson
"Novel
                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing;
SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                          VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
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D28769; BAA05958.1; -.
J U89336; AAB47491.1; -.
J AB056432; BAA89369.1; -.
J AJ133822; CAB43108.1; -.
J AF280289; AAG35728.1; -.
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10; Conserv
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IPR003598; Ig_c2.
IPR003600; Ig_like.
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N-LINKED (GLCNAC. ..) (
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
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ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
PGPGDDGRPGDSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
                                                                                                                                                                                    GVPLPLPPSPVLILPEIGPQDQGTYSCVATHSSHGPQESRA VSISIIEPGEEGPTAGSVGGSGLGTLALALGILGGLGTAAL
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                                                                                  /FTId=VAR_011338.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RI
(RECEPTOR FOR ADVANCED GLYCOSYLATION END PROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006;
InterPro; IPR003598;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
"Recombinant advanced glycation end product receptor pharmacokinetics in normal and diabetic rats.";
wol. pharmacol fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renard C., Chappey O., Wautier M.P., Morser J., Zhao L., Schmidt A.M., Sci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung; MEDLINE=97368045; PubMed=9224812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAGE_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATE IN DIABETES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
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                                                                                                                                                                                                                                                                                                                                                                     Processing SM00408; IGC2; ... SM00408; IG_like; 1...; SM00410; IG_like; 1... SM00410; IG_MHC; SM00410; IG_MHC;
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Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                               . 1.
1
         MW;
CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.

1 (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                         SPECIFIC RECEPTOR
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                             ADVANCED GLYCOSYLATION END PRODUCT
                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
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Query Match Best Local S Matches 9

Similarity 9; Conserv

Conservative

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SEQUENCE
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Q62151;
Q1-NOV-1997
                                                                         DOMAIN
DOMAIN
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DOMAIN
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TRANSMEM
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SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTO (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                               MGD;
                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renard C., Chappey O., Wautier M.P., Nagashima M., Lu
Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wa
"Recombinant advanced glycation end product receptor
in normal and diabetic rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C; TISSUE=Lung;
MEDLINE=97368045; PubMed=9224812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
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                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                                                                                                                                                                                   [mmunoglobulin
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); MGI:893592; Ager.

terpro; IPR003006; Ig_MHC.

Terpro; IPR003598; Ig_c2.

Terpro; Terpro3500; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: ENDOTHELIAL CELLS. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. 2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATE
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Eutheria;
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                                                                                                                                                                                   domain;
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Rodentia;
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   MW.
                                                         POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.
N-LINKED (GLCNAC. . N-LINKED (GLCNAC. . 1279796FD1579357 )
                                    POTENTIAL.
                                                                                                                                             ADVANCED GLYCOSYLATION END PRODUCT-
SPECIFIC RECEPTOR.
                                                                                                                                EXTRACELLULAR (POTENTIAL).
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Sciurognathi; Muridae;
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                                                                                                                                                                               Transmembrane; Signal
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                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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                                                                      DOMAIN 1.
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Wautier
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Murinae; Mus
            (POTENTIAL)
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Best Local
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                                                                                                                                                         InterPro: IPR003600; Ig_111
Pfam; Pf00047; ig; 2
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_11ke; 1
PROSITE; PS00290; IG_MHC; :
           DISULFID
DISULFID
CARBOHYD
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Q28173;
Q1-NOV-1997
                                          DOMAIN
DISULFID
                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              Neeper M., Schmidt A.M., Brett J., Yan S.I Elliston K., Stern D., Shaw A.; "Cloning and expression of a cell surface glycosylation end products of proteins."; J. Biol. Chem. 267:1498-15004(1992).
                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _BOVIN
   CARBOHYD
                                                                                                                                                                                                                                                                                                                   This
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01-NOV-1997 (Rel. 35, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCTS - SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                             TRANSMEM
                                                                                                        DOMAIN
                                                                                                                                       SIGNAL
                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                  EMBL; M91212; AAA03575.1;
                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROT-!- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN
2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92340547; PubMed=1378843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGER OR RAGE
                                                                                                                                                [mmunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                           WHICH ACCUMULATE IN VASCULAR
                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Bovine).
 353
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                                                                                                                                              domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%;
                                                                                                                                               Glycoprotein; Transmembrane;
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                              POTENTIAL. POTENTIAL.
                                                  CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
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N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                            EXTRACELLULAR POTENTIAL.
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                                                                                                                  RECEPTOR
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P44688;
01-NOV-1995
                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=95350630; PubMed=7542800;
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20-AUG-2001
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FUNCTION: SEQUENCE-SPECIFIC
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                                                                                         ITARIGE 171
                                                                                                                      ITARIGE
                                                                                                                                                                                                                                                                                                U32723; AAC22062.1; P06722; 2AZO.
                                                                                                                                                        Similarity 7; Conserv
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                                                                                                                                                                                                                                            Hydrolase; Endonuclease; Complete pi
223 AA; 24906 MW; 339A4EF9DA0E622A
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01-OCT-1996
01-NOV-1997
20-AUG-2001
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TRANSMEM
SEQUENCE
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between the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RD
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Bacteria; Proteobacteria;
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Hypothetical protein; Transport; Amino-i
                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                                                                                                                Hypothetical
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Conservative
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L AMINO-ACID ABC TRANSPORTER PERMEASE
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Amino-acid
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   234
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                                                                                                                                                                           DB
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Dougherty B.A., Merrick J.M.,
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ng as its content is in
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Best Local S
Matches 6
                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=138-2;

MEDLINE=97137009; PubMed=8982386;

MEDLINE=97137009; PubMed=8982386;

Nakamura T., Katch Y., Shimizu Y., Matsuba Y., Unemoto T.;

"Cloning and sequencing of novel genes from Vibrio alginolyticus

"Cloning and sequencing of novel genes from Vibrio alginolyticus

"Cloning and sequencing of novel genes from Vibrio alginolyticus

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"Cloning and sequencing of novel genes from Vibrio alginolyticus

"Control of the sequencing of the sequence of t
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MEDLINE-84270667; PubMed-6087149;

Baer R., Bankier A.T., Biggin M.D., De
Gibson T.J., Hatfull G., Hudson G.S.,

Tuffnell P.S., Barrell B.G.;

Tuffnell P.S., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epstein-barr virus (straviruses, Viruses, dsDNA viruses,
                                              This
                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio alginolyticus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROC_VIBAL P52053;
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                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA sequence and expression of the B95-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
                                                                                                      chim. Biophys. Acta 1277:201-208(1996).
CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+)
CARBOXYLATE + NAD(P)H.
CARBOXYLATE + NAD(P)H.
PATHWAY: TERMINAL (THIRD) STEP IN PROLINE
SIMILARITY: BELONGS TO THE PYRROLINE-5-CAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; V01555; CAA24835.1;
A03787; QQBE43.
S33040; S33040.
                      SWISS-PROT entry is copy
een the Swiss Institute
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(Rel. 34, Last sequence update)
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-CARBOXYLATE REDUCTASE (EC 1.5.1
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Bioinformatics
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uses, no RNA stage;
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23791 MW;
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                      copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation -
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Pred. No. 4.5
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1.5.1.2)
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outstation -
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Lyase; Glycolysis; MACT\_SITE 146 1
METAL 233 2
METAL 274 2
METAL 301 3
SEQUENCE 401 AA;

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20-AUG-2001 (Rel. 40, Las
20-AUG-2001 (Rel. 40, Las
20-AUG-2001 (Rel. 40, Las
ENOLASE (EC 4.2.1.11) (2:
GLYCERATE HYDRO-LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1728;
STRAIN=DAM 1728;
MEDLINE=20479972; PubMed=11029001;
MEDLINE=20479972; PubMed=11029001;
Member A., Graml W., Santos-Martinez M.-L., Koretke Ruepp A., Graml W., Stocker S., Lupas A.N., Fushman D., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENO_THEAC Q9HJT1;
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formaticial transfer is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence of the thermoacidophilic so
acidophilum.";
Nature 407:508-513(2000).
-i- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; pF01089; P5CR; 1.
pROSITE; PS00521; P5CR; 1.
Oxidoreductase; Proline biosynthesis; NADP.
SEQUENCE 278 AA; 29815 MW; 50359E5EF97CD68B CRC64;
                                                                                                                           prodom; PS00164; ENOLASE; PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email t
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                                                                                                                                                                                                EMBL; AL445065; CAC12011.1; -.
InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb~sib.ch).
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-!- COFACTOR: MAGNESIUM IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                - ! - SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
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30-MAY-2000 (Rel. 3
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15-JUL-1998 (Rel. 3
20-AUG-2001 (Rel. 4
HYPOTHETICAL 48.5 M
                                                                                       METTH
 Methanobacterium thermoautotrophicum
                                                                 ARLY_METTH 026369;
                                                                                                                                                                                                                                Hypothetical protein; Zinc-finger; DNA-binding; Nuclear ZN_FING 26 64 MYND-TYPE. SEQUENCE 429 AA; 48546 MW; 51F223A6D0B56BA9 CRC64;
                                                                                                                                                                                                                                                                                     EMBL; Z46794; CAA86783.1; -. WormPep; R06F6.4; CE16303.
                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID-6239;
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Q09415; Q09414;
Q1-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
             ARGH OR
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Pfam; PF01753; Zf-MYND;
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20-AUG-2001
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J. Bacteriol. 179:7135-7155(1997).
J. Bacteriol. 179:T135-7155(1997).
J. Bacteriol. STEP IN ARGINING BIOSYNTHESIS.
STRAIN-MADRID E;
MEDLINE-97419517; PubMed-9274032;
Andersson J.O., Andersson S.G.E.;
"Genomic rearrangements during evolution of the
intracellular parasite Rickettsia prowazekii as
analysis of 52015 bp nucleotide sequence.";
Microbiology 143:2783-2795(1997).
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PRINTS; PR00145; DCRYSTALLIN.
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PROSITE; PS00163; FUMARATE_LYASES; FALSE_NEG
Arginine biosynthesis; Lyase; Complete protections of the protection of the p
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                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                           Rickettsiaceae;
NCBI_TaxID=782;
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Bacteria; Proteobacteria;
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InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR002106; ARA_TRNA_LIGASE_II.
InterPro; IPR002320; tRNA-Synt_thr.
InterPro; IPR002320; tRNA-Synt_Thr.
Pfam; PF00587; tRNA-Synt—2b; 1.
PRINYS; PR01047; TRNASYNTHTIR.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FA
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
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01-NOV-1995 (Rel. 32, Created)
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RECCOMBINATION PROTEIN 2.
REC2 OR REC-2 OR HI0061.
Haemophilus influenzae.
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DOMAIN 242
METAL 333
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SEQUENCE 635 A
MEDILINE-9431577; PubMed=8063112; Clifton S.W., McCarthy D., Roe B.A.; "Sequence of the rec-2 locus of Haemophilus influenzae: comE-ORF3 of Bacillus subtilis and msbA of Escherichia c Gene 146:95-100(1994).
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-!- CATALYTIC ACTIVITY: ATP + L-THREONINE PYROPHOSPHATE + L-THREONYL-TRNA(THR).
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Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin
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Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Tine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
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Science 269:496-512(1995).
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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U32691; AAC21739.1;
HI0061; -.
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P45997;
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01-NOV-1995
01-NOV-1995
                                                                                                             SEQUENCE FROM N.A.

STRAIN-AM30 (770235) / SEROTYPE B;

STRAIN-S089703; PubMed-7997179;

Wan Ham M.S., van Alphen L., Mooi F.R., van Putten J.P.;

"The finbrial gene cluster of Haemophilus influenzae type b.";

MOI. Microbiol. 13:673-684(1994)

-1- FUNCTION: ESSENTIAL FOR PILIATION.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
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Bacteria; Proteobacteria;
Haemophilus.
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Infect. Immun. 62:468-475(1994).
-!- FUNCTION: ESSENTIAL FOR PILLATION
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STRAIN-EAGAN / SEROTYPE B;
MEDLINE-94131580; PubMed-7905461;
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                                                                                                                                                        Pfam; PF00577; Usher; 1.
PROSITE; PS01151; FIMBRIAL_USHER; 1.
Outer membrane; Transmembrane; Fimbria; Transport;
                                                                                                                                                SIGNAL
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                                                                                                                                                                                                 InterPro;
253 TARIGE 258
                       5
                       TARIGE 10
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                                                          Similarity
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92641 MW;
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Pred.
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Copyright (c) 1993 - 2000 Com
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23.057 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	% Query Match	Query Match Length DB	DB	ID	Description
ъ	10	100.0	342	4-	Q9Y3R3	Q9y3r3 homo sapien
2	9	90.0	402	11	035444	
ω	0	60.0	32	6	Q9TRQ1	Q9trq1 bos taurus
4	6	60.0	127	12	Q9EAJ5	Q9eaj5 human immun
J	6	60.0	298	10	Q9ZS04	Q9zs04 arabidopsis
o	o	60.0	389	9	Q38644	Q38644 bacteriopha
7	o	60.0	452	10	Q9LRM5	Q91rm5 arabidopsis
8	O	60.0	471	ш	Q04928	Q04928 methanobact
9	. 6	60.0	548	10	Q9SVE2	Q9sve2 arabidopsis
10	6	60.0	609	10	Q9SHB9	Q9shb9 arabidopsis
11	6	60.0	822	ν	Q9L273	Q91273 streptomyce
12	6	60.0	837	2	P94813	P94813 haemophilus
13	U	50.0	39	2	Q9RFA3	Q9rfa3 xenorhabdus
14	v	50.0	68	ນ	Q52235	Q52235 clostridium
15	u	50.0	71	4	Q9NPY6	Q9npy6 homo sapien
16	u	50.0	72	11	Q9CZU1	Q9czul mus musculu
17	ر د	50.0	. 72	1	Q9CR64	Q9cr64 mus musculu
18	5	50.0	74	ۍ.	Q9VWH8	Q9vwh8 drosophila
19	տ	50.0	77	4	Q9BZT4	

Conservative

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Q9jn73 streptomyce	041952 murid herpe 09hr46 halohacteri	064393 triticum ae	Q9f3h0 streptomyce	Q51542 pseudomonas	064392 triticum ae	P93180 hordeum vul	Q9zsl4 cichorium i		Q9ck57 pasteurella	=			Q9ihw2 human immun	Q9hzal pseudomonas	Q9sqg3 triticum ae	Q9sqg4 triticum ae	Q9ryp1 deinococcus	Q9are8 lithospermu	Q9y517 homo sapien	human	Q992f8 human immun	Q9ixr2 human immun	human	Q98xx4 human immun

## ALIGNMENTS

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RESULTATION OF THE PROPERTY OF
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                          Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; Schuler A., Huber G.; "cDNA cloning of a novel secreted isoform of the human Receptor for Advanced Glycation End products (RAGE) and characterization of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Y3R3
                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ133822; CAB43108.1; -.
                                                                                                                                                                                                                                                                                                                                              Receptor.
                                                                                                                                                                                               342 AA;
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                                                                                                                                                                                                                                                                      22
342
                                   100.0%; Score 10; DB 4; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                               36193 MW;
                                                                                                                                                                   POTENTIAL.

RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS.

; 35DDF66A13E39B38 CRC64;
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Best Local S
Matches 9
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Q9TRQ1;
01-MAY-2000
01-MAY-2000
01-JUN-2000
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035444;
01-JAN-1998
01-JAN-1998
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Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                        Schmidt A.M., Vianna M., Gerlach M., Brett J., Ryan J., Kao J., Esposito C., Hegarty H., Hurley W., Clauss M.; "Isolation and characterization of two binding proteins for advanced glycosylation end products from bovine lung which are present on the endorthelial cell surface."; J. Biol. Chem. 267:14987-14997(1992). SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_LIKe; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 402 AA; 42653 MW; DBFDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
ROWEN L., MANAIRAS G., Qin S., Ahearn
Loretz C., Schmidt S., Tipton S., Trai
Submitted (CCT-1997) to the EMBL/GenBB
-1- SIMILARITY: TO IMMUNOGLOBULIN AND
                                                                                                                                                                                                                                                             MEDLINE=92340546; PubMed=1321822;
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                       SEQUENCE
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-MAY-2000 (TERMBLrel. 13, Last sequence update)
-JUN-2000 (TERMBLrel. 14, Last annotation update)
KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      werPro; IPR003600; Ig_like.
erPro; IPR003006; Ig_like.
erPro; IPR003006; Ig_MHC.
m; PF00047; ig; 3.
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  6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conserv
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60.0%;
nilarity 100.0%;
Conservative
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Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Qin S., Ahearn M.E., Dankers C., Lasky S.,
., Tipton S., Traicoff R., Zackrone K., Hood L.;
to the EMBL/GenBank/DDBJ databases.
MMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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05,
17,
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Score 6; DB 6
Pred. No. 4.7
0; Mismatches
    0;
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Pred. No. 0.0
0; Mismatches
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Last sequence update)
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Sciurognathi; Muridae;
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minantia; Pecora; Bovoidea
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                        7.6
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01-MAY-1999
01-JUN-2001
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01-MAR-2001
01-JUN-2001
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NON_TER
                 STRAIN-CV. COLUMBIA;
MEDLINE-99081866; PubMed-9862990;
AUBOUTY S., Kreis M., Lecharny A.;
"The DEAD box RNA helicase family in Arabidopsis
"Uncleic Acids Res. 27:628-636(1999).
-!- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
EMBL; AJ010468; CAA09207.1; -.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AJ296662; CAC03693.1; -
Interpro; IPR001969; Asp_protease.
Interpro; IPR001995; Asp_prot_retrov
Pfam; PF00077; rvp; 1
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Barlow K.L., Tatt I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency Viruses; Retroid viruse NCBI_TaxID=11676;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                     RNA HELICASE
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39 ITARIG
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nes 6; Conserv
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Best I
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       Hayashi T., Matsumoto H., Ohnishi M., Terawaki Y.;
"Molecular analysis of a cytotoxin-converting phage, p
pseudomonas aeruginosa: structure of the attp-cos-ctx
integration into the serine tRNA gene.";
Mol. Microbiol. 7:657-667(1993).
EMBL; S75107; AAD14164.1; -.
EMBL; D13409; BAA02675.1; -.
EMBL; S75107; AAD14165.1; -.
EMBL; Y13918; CAA74224.1; -.
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01-NOV-1996 (TrembLrel.
01-NOV-1996 (TrembLrel.
01-JUN-2001 (TrembLrel.
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SEQUENCE
                                                                                                                                                                                                                   phage; phiCTX.";
Submitted (OCT-1997)
[5]
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-PHICTX-C;
                                                                                                                                                                                                                                                                                                                                                                                    Wang Z., Xlong G., Lutz F.;
"Site-specific integration of the phage phi CTX genome Pseudomonas aeruginosa chromosome: characterization of integrase gene located close to and upstream of attp."; Mol. Gen. Genet. 246:72-79(1995).
                                                                                                                                           "Pseudomonas aeruginosa cytotoxin: and the mechanism of activation of Mol. Microbiol. 3:861-868(1989).
                                                                                                                                                                          MEDLINE=90014160; PubMed=2507866; Hayashi T., Kamio Y., Hishinuma F
                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=PHICTX-C;
                                                                                                                                                                                                                                  "Whole genome sequence of phage; phiCTX.";
                                                                                                                                                                                                                                                                                                                                             Hayashi T.,
Submitted (
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                                                                                       MEDLINE=93225809; PubMed=8469112;
Hayashi T., Matsumoto H., Ohnishi
                                                                                                               STRAIN-PHICTX-C
                                                                                                                         SEQUENCE FROM
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MEDLINE=95124301; PubMed=7823914;
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AB008550;
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BAA36272.1;
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Pred. No. 32;
0; Mismatches
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No.
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01-OCT-2000
01-OCT-2000
                                                              Q04928 PRELIMINARY; PRT; Q04928; O1-NOV-1996 (TrEMBLrel 01, Created) O1-NOV-1996 (TrEMBLrel 01, Last seq 01-JUN-2001 (TrEMBLrel 17, Last ann HYPOTHETICAL 51.6 KDA PROTEIN (ORF5)
                                                                                                                                                                                                                                               Lyase.
SEQUENCE
                                                                                                                                                                                                                                                        InterPro; IPR002022; Amballergen. Pfam; PF00544; pec_lyase; 1. PRINTS; PR00807; AMBALLERGEN. Lyase.
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Pfam; PF00589; Phage_integrase;
SEQUENCE 389 AA; 44431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ea
Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
SEQUENCE FROM N.A. MEDLINE=93341463; PubMed=8393514;
                                    Archaea; Euryarchaeota; Methanothermobacter.
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                            NCBI_TaxID=145262;
                                                         Methanobacterium thermoautotrophicum
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                                                                                                                                                                                                                                                                                                                                            Nakamura
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Matches 6
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Q9SHB9;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL035539; CAB37499:1; -
EMBL; AL161593; CAB80508.1; -
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermsids II, Brassicales; Brassicaceae; Arabi
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Q9SVEZ;
Q9SVEZ;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 60.8 KDA PROTEIN.
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Wedler H., Kutzner M.,
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Mayer K.F
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"Distribution and characterization of plasmid-related sequences chromosomal DNA of different thermophilic Methanobacterium strains
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(FEB-1999) to the EMBL/GenBank/DDBJ databases
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RALLING COLUMNIA.

RX MEDLINE-20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Fujii C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Woffat K.S.,

RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;

RA Salzberg S.L., Fraser S.L., Manara M.C., White O., Elsen J.A.,

RA Salzberg S.L., Fraser S.L., Washama W.C., White O., Elsen J.A.,

RA Salzberg S.L., Fraser S.L., Washama W.C., White O., Elsen J.A.,

RA Salzberg S.L., Fraser S.L., Washama W.C., White O., Elsen J.A.,

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NCBI_TaxID=3702;
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Seeger K.J., Harris !
Submitted (JAN-2000)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
HYPOTHETICAL 91.7 KDA PROTEIN.
STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapa
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a d
                                                                                                                                                                                                                                      STRAIN=A3(2);
Cerdeno A.M.,
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                                                                                                                                                                                                      , Parkhill J., Ba
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EMBL/GenBank/DDBJ databases.
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J. Bacteriol. 178:6564-6570(1996).
EMBL: U54780; AAB70873.1; -
InterPro; IFR000015; Fimb_usher.
Pfam; PF00577; Usher; 1.
PROSITE; PS01151; FIMBRIAL_USHER; 1.
SEQUENCE 837 AA; 92683 MW; 6F01ED1D2FFC4176
SEQUENCE FROM N.A.
STRAIL-ATCC19061;
VIVAS E.I., Goodrich-Blair H.;
"rpoS is necessary for Xenorhabdus nematophilus nematode host, Steinernema carpocapsae.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ da
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Hypothetical protein
SEQUENCE 822 AA;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                Xenorhabdus nematophilus.
Bacteria; Proteobacteria;
Xenorhabdus.
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NCBI_TaxID=727;
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01-MAY-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Best Local :
                                                                             Laird G.;
Submitted (AUG-2000) |
EMBL; AL117333; CAC01!
NON_TER 71 7;
SEQUENCE 71 AA; 77;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ631M13.1 (SIMILAR TO MOUSE SELLL (SEL-1 (SUPPRESSOR
                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                 C.ELEGANS)-LIKE).)
DJ631M13.1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLASMID PNB2 (FROM CLOSTRIDIUM THERMOSACCHAROLYTICUM)
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Search completed: April 24, 2002, 09:24:28 Job time: 252 sec Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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11.176 Million cell updates/sec
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ш.	Human prostate tum	nebact	Rape seed beta-ket	Rape leaf beta-ket	Corynebacterium gl	<b>.</b>	Peptide #8843 enco	Cephalosporin anti	Amino acid sequenc	Chlamydia pneumoni	_				Stachybotrys chart	Chlamydia pneumoni	E. coli growth and	DP3A	E. coli DP3A prote	0					M. smegmatis InhA.	Plant retroelement	nal s	Bovine RAGE V-doma	Rat RAGE V-domain	0	Extracorporeal cir	RAGE pol	Human soluble rece

## ALIGNMENTS

AAY09353

AAY09353 standard; peptide;

10 AA

AAY09353;

09-JUL-1999 (first entry)

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Human RAGE V-domain peptide SEQ ID NO:5.

RAGE; V-domain; receptor for advanced glycation endproduct;
ligand binding site; amyloid-beta; Alzhelmer's disease; Down's syndrome; senility; renal failure; hyperlipidaemic atherosclerosis; dementia; neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.

Homo sapiens.

W09918987-A1.

22-APR-1999.

09-OCT-1998; 98WO-US21346.

09-OCT-1997; 97US-0948131.

(UYCO) UNIV COLUMBIA NEW YORK.

Lamster I, Schmidt AM, Stern D, Yan SD;

WPI; 1999-277439/23.
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(C (ABP) interaction with a receptor for RAGE when the receptor is on the
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
CC extracellular assembly of an ABP into a fibril; (5) inhibiting
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
CC of a microglial cell into senile plaques; (7) inhibiting activation of a
CC microglial cell by an ABP; (8) treating a subject with a condition
CC associated with an interaction of an ABP with a receptor for RAGE on a
CC cell; (9) evaluating the ability of an agent to inhibit binding of an
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
CC ABP with a receptor for RAGE on the surface of a cell; (10)
CC with a receptor for RAGE when the receptor is on the surface of a cell;
CC with a receptor for RAGE when the receptor for RAGE on a cell with an interaction of an RAGE with a receptor for RAGE on a cell rhe methods
CC and be used for treating conditions associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods
CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an RAGE with a receptor for RAGE on a cell with an interaction of an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a receptor for RAGE on a cell with an interaction of an CC ABP or an RAGE with a cell with an interaction of an RAGE with a cell w
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                                             Schmidt AM,
                                                                                                                                  17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human Receptor to AGE (RAGE) amino acid sequence fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY52135
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                                                                                                                                                                           16-APR-1999;
                                                                                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                 W09954485-A1
                                                                                                                                                                                                                                                                                                          Homo sapiens
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2000-013260/01
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                                                                                     COLUMBIA NEW YORK
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                                                                                                                                                                                                     when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts was range of physiologically and pathophysiologically relevant ligands
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts -
                                                             Local
                                       l Similarity 100
10; Conservative
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                                                                                                                                         23-OCT-1997.
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                  diabetes mellitus.
                                                                                                                                                                                                            Human soluble RAGE immunologically active fragment SEQ ID NO:12
                                                                                                                                                                                                                                        AAW44208;
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                                                                                                                                                                                       n; soluble receptor; advanced glycosylation end product; RAGE;
antibody; vascular permeability; immunologically active fragment;
                                                                                                                                                                                                                          (first entry)
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The present sequence represents an immunologically active fragment of a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes

Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus

WPI; 1997-558580/51 Hollander DA, 16-APR-1996;

96US-0633148 97WO-EP01834

(SCHD ) SCHERING PATENTE

ΑG

Morser MJ,

Nagashima

11-APR-1997;

Claim 2; Page 46; 90pp; English.

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RESULT
AAW33762
ID WAW33762
XX AAW3
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Matches 10
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                          retinopathy) or haemodialysis-associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture at to screen for compounds that are agonists and antagonists of AGE/RAGE
                                                                                                                                                                                                                  This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active fragments or their mimetics can inhibit interaction between advanced glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                        disorders such as neuropathy, nephropathy, atherosclerosis or
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   interaction.
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diabetes mellitus; treatment; atherosclerosis;
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Pred. No.
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hes 0;
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                                    product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for associated amyloidosis or atherosclerosis. The Ab can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                            Anti-advanced glycosylation end product polypeptide antibody prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
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Sequence
                                                                                                                                                                                                     The present sequence represents an immunologically active fragment
                                                                                                                                                                                                                                 Claim 2; Page 49; 90pp;
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                                                                                                                                                                                       soluble human receptor to an advanced glycosylation
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                            purification of human
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immunologically active fragment;
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Local

Similarity

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RESULT
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ID AAW3
                                                                                                    This is a peptide fragment of a human advanced glycosylation end-product receptor (RAGE) polypeptide. The RAGE polypeptides and its active CC fragments or their mimetics can inhibit interaction between advanced CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They CC are used to treat diseases associated with AGE/RAGE interaction, such as CC increased vascular permeability, diabetes mellitus (particularly CC complications such as micro- vasculopathy or occlusive vascular CC disorders such as micro- vasculopathy or occlusive vascular CC cretinopathy) or haemodialysis-associated amyloidosis, also activation CC of microgilal cells by beta-amyloid peptides in Alzaheimer's disease or age-related disorders such as oxidative stress. These RAGE polypeptides CC are also used, when immobilised, to purify AGE from a protein mixture and to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal CC levels of AGE. Antibodies against RAGE polypeptides are useful as CC interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
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                                                                                                   Sequence
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AQNITARIGE 10
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                           l Similarity
10; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagashima
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                                        100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end-product receptor; RAGE; screening; AGE;
diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment 14.
                                        . 0 %
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                                      Score 48;
Pred. No.
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                          Mismatches
                                      DB 18;
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RESULT
AAY09349
ID AAY0
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                                                                                                                                                                                                                                                                                                The present invention describes novel isolated peptides (I) having an CC amino acid sequence corresponding to an amino acid sequence of a CC v-domain of a receptor for an advanced glycation end product (RAGE). CC Also described are methods for: (1) inhibiting an amyloid-beta peptide CC (ABP) interaction with a receptor for RAGE when the receptor is on the CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) inhibiting formation of an ABP fibril on a cell; (4) inhibiting cell; (3) CC extracellular assembly of an ABP into a fibril; (5) inhibiting infiliration of aggregation of ABP on the surface of a cell; (6) inhibiting activation of a cegaration of a microglial cell into senile plaques; (7) inhibiting activation of a CC microglial cell by an ABP; (8) treating a subject with a condition cassociated with an interaction of an ABP with a receptor for RAGE on a cell; (9) evaluating the ability of an agent to inhibit binding of an CC cell; (9) evaluating the ability of an agent to inhibit binding of an CC ABP with a v-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a subject; (12) inhibiting an RAGE's interaction cut in the surface of a cell; (11) inhibiting an each of a cell; (11) inhibiting an each of a cell; (12) inhibiting an RAGE's interaction cut in the surface of a cell; (13) treating a subject; (12) inhibiting an RAGE's interaction cut in the surface of a cell; (13) treating a subject; (14) inhibiting an RAGE's interaction cut in the surface of a cell; (12) treating a subject with a condition associated with an exceptor is on the surface of a cell; (13) treating a subject with a condition associated with an exceptor is on the surface of a cell; (13) treating an each of a cell; (14) treating an each of a cell; (15) the condition and cell; (16) the condition associated with an exceptor is on the surface of a cell; (17) treating and the cell into the cell into the surface of a cell; (18) the cell into the cell into the cell into the cell into the cell in
                                                                                                                                                                         and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of a ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's disease, senility, renal failure, hyperlipidaemic atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; amyloidosis; autoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                   an autoimmune disease, inflammation, a tumour, cancer, male impotence,
                                                                                                                           neuronal cytotoxicity, Down's syndrome, dementia associated with trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides based on an advanced glycation useful for treating Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-277439/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal cytotoxicity; head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     senility; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RAGE V-domain peptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding site; amyloid-beta; Alzheimer's disease; Double ty; renal failure; hyperlipidaemic atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 78; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                           periodontal disease, neuropathy, retinopathy, nephropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0948131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trauma; amyotrophic lateral sclerosis;
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                                                                                                                           amyloidosis,
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Matches Query Match Best Local S

10;

Conservative

Similarity

100.0%; So 100.0%; P ative 0;

Score 48; Pred. No. Mismatches

DB 20; 0.0021;

Length 30; Indels

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                                                                 Query Match
Best Local
                                                    Matches
                                                                                                                                                   This is the amino acid sequence of a fragment of the human soluble Receptor for Advanced Glycation Endoproducts (RAGE). RAGE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting tumour invasion or spreading by administration receptor for advanced glycation endproducts \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-013260/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble receptor for advanced glycation endproducts; RAGE; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY52134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY52134 standard; protein; 30 AA.
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                        1 AQNITARIGE 10
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aqnitarige
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor
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                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                         Page 62; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis; amphoterin; neuron; inhibit;
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                                                   Conservative
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                                                 Score 48; DB Pred. No. 0.0; Mismatches
                                                              DB 21;
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                                                                          Length 30;
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RESULT

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AAW44200
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AC AAW4
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Huma
KW Huma
KW AGE;
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YM WO9
FT W1sc
FT W1
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ID AAW:
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AC AAW:
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AC AAW:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a mature human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, haemodialysis associated amyloidosis or atheroscierosis. The Ab can also be used for the content of th
    Human RAGE polypeptide (318 amino acid residues).
                                                                                08-MAY-1998 (first entry)
                                                                                                                                                            AAW33754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            permeability, useful to treat diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV12395
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                                                                                                                                                                                                                                         AAW33754 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the isolation and purification of human RAGE polypeptide.
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| 1 agnitarige 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular permeability; diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0633148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by CCT"
                                                                                                                                                                                                                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 318;
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RESULT 1
     TX SX TX TX XX X
                                                                                                                                                                                                                                                                                                                                                                                 This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (318 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC disorders such as neuropathy, nephropathy, retinopathy or

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC are also used, when immobilised, to purify AGE from a protein mixture and

CC to screen for compounds that are agonists and antagonists of AGE/RAGE

CC interaction. They can also be used diagnostically to detect abnormal

CC interaction between AGE and RAGE or other receptors and for purification

CC interaction between AGE and RAGE or other receptors and for purification

CC and quantification of RAGE polypeptides. The encoding nucleic acids are

CC used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                 AAY52130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Advanced glycosylation vascular permeability; Alzheimer's disease.
           Soluble receptor for advanced glycation endproducts; RAGE; tumour;
                                                 Human Receptor to
                                                                                  28-JAN-2000
                                                                                                                                               AAY52130 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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invasion; metastasis; amphoterin; neuron; inhibit; therapy
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                                                                                                                                                                                                                                                               1 AQNITARIGE
                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                 Conservative
                                                                                 (first entry)
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                                             AGE (RAGE) amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end-product receptor; RAGE; screening; AGE;
diabetes mellitus; treatment; atherosclerosis;
                                                                                                                                                                                                                                                                                                               .09;
                                                                                                                                                 332 AA.
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                0.03;
                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                              Length 318;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                              Gaps
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Query Match
Best Local Similarity
                                                                                                           This is the amino acid sequence of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE colocalizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AAY52132-Y52135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable
                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10-11;
                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting to receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-013260/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             tumour invasion or spreading by administration of soluble
or advanced glycation endproducts -
                                                                 332
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                                                                 Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0062365
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                              88pp; English.
               .0%;
 Score 48; I
Pred. No. 0.
                 DB
.031;
               21;
               Length 332;
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AAW44199
                                                                                                                                                                                                                                                                  RESULT
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                            23-OCT-1997
                                                       W09739125-A1
                                                                                 Homo sapiens
                                                                                                           Human; soluble
AGE; antibody;
                                                                                                                                                      Human
                                                                                                                                                                                 14-MAY-1998
                                                                                                                                                                                                             AAW44199;
                                                                                                                                                                                                                                       AAW44199 standard; Protein; 340
11-APR-1997;
                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                    1 AQNITARIGE 10
                                                                                                                                                                                                                                                                                                          1 agnitarige 10
                                                                                                                                                     soluble
                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                (first entry)
                                                                                                                                                     receptor to an
                                                                                                             receptor; advanced glycosylation end product; RAGE; vascular permeability; diabetes mellitus.
 97WO-EP01834
                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                     advanced glycosylation end product.
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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16-APR-1996;

96US-0633148

(SCHD ) SCHERING PATENTE

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RESULT 1
AAW33753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, neemodialysis associated amyloidosis or atheroselerosis. The Ab can also be used for the control of t
                New soluble advanced glycosylation end-product receptor polypeptide - used for reducing vascular permeability, complications of diabetes etc., also for purification and to screen for modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Advanced glycosylation vascular permeability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW33753 standard; Protein; 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                         N-PSDB;
                                                                                                                                                                      Morser MJ,
                                                                                                                                                                                                                                                             16-APR-1996;
                                                                                                                                                                                                                                                                                                         11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                    23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                             WO9739121-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW33753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the isolation and purification of human RAGE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-advanced glycosylation end product polypeptide antibody
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                                                                                                                                                                                                                  (SCHD ) SCHERING AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AQNITARIGE 10
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DB; AAV12394.
                                                                                                      1997-526458/48
DB; AAV06517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 40-41; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                      Nagashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                             96US-0633147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end-product receptor; RAGE; screening; AGE;
diabetes mellitus; treatment; atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid residues).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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RESULT
AAB8192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                    Material for extracorporeal circulation, applicable in selective elimination of diabetic complication factors such as carbonyl stress products caused by abnormally promoted carbonyl stress from excretor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to screen for compounds that are agonists and antagonists of AGE/RAGE interaction. They can also be used diagnostically to detect abnormal levels of AGE. Antibodies against RAGE polypeptides are useful as immunoassay reagents for measurement of RAGE levels, and as inhibitors of interaction between AGE and RAGE or other receptors and for purification and quantification of RAGE polypeptides. The encoding nucleic acids are used to express recombinant RAGE and as probes for isolating related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosylation end-products (AGE) and a receptor (specifically RAGE). They are used to treat diseases associated with AGE/RAGE interaction, such as increased vascular permeability, diabetes mellitus (particularly complications such as micro- or macro- vasculopathy or occlusive vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is a human advanced glycosylation end-product receptor (RAGE) polypeptide (340 amino acid residues). The RAGE polypeptides and its active fragments or their minetics, inhibit interaction between advanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                age-related disorders such as oxidative stress. These RAGE polypeptides are also used, when immobilised, to purify AGE from a protein mixture are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis) or haemodialysis-associated amyloidosis, also activation of microglial cells by beta-amyloid peptides in Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 1A; 91pp; English.
                                            Claim 1; Page 31-32;
                                                                           dysfunction
                                                                                                                                                     WPI; 2001-290314/30.
                                                                                                                                                                                  Shimizu S,
                                                                                                                                                                                                              (TORA ) TORAY IND INC
                                                                                                                                                                                                                                              08-SEP-1999;
                                                                                                                                                                                                                                                                             08-SEP-2000; 2000WO-JP06172
                                                                                                                                                                                                                                                                                                           15-MAR-2001
                                                                                                                                                                                                                                                                                                                                        WO200118060-A1
                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                     diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                  Extracorporeal circulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracorporeal circulation material receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 404
                                                                                                                                                                                                                                                                                                                                                                                                     vascular
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                                                                                                                                                                                  Kubota M,
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                                                                           in vascular
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                                         36pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                  carbonyl stress product; receptor; excretory dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                  Η,
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The present invention describes a material for extracorporeal which is made from a water-insoluble carrier immobilized with

circulation a protein

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The present invention describes novel isolated peptides (I) having an cannot acid sequence corresponding to an amino acid sequence of a CV domain of a receptor for an advanced glycation end product (RAGE).

Also described are methods for: (1) inhibiting an amyloid-beta peptide (RABP) interaction with a receptor for RAGE when the receptor is on the surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3) inhibiting formation of an ABP fibril on a cell; (4) inhibiting cell; (3) continuity of an ABP into a fibril; (5) inhibiting infiltration aggregation of ABP on the surface of a cell; (6) inhibiting infiltration of a microglial cell into senile plaques; (7) inhibiting activation of a massociated with an interaction of an ABP with a receptor for RAGE on a cell; (9) evaluating the ability of an agent to inhibit binding of an ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10) inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                            Claim 3; Page 78; 101pp; English.
                                                                                                                                                                                                                                                                                                              New peptides based on an advanced glycation end product receptor useful for treating Alzheimer's disease and Down's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis; multiple sclerosis; amyloidosis; aucoimmune disease; inflammation; tumour; cancer; male impotence; wound healing; periodontal disease; neuropathy; retinopathy; nephropathy; neuronal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand binding site; amy senility; renal failure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY09350;
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                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor for advanced glycation endproduct; site; amyloid-beta; Alzheimer's disease; Dow
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Query Match
Best Local Similarity
""+"hes 9; Conserv
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                                                                                                                                                                                         periodontal disease in a subject; (12) inhibiting an RAGE's interaction with a receptor for RAGE when the receptor is on the surface of a cell; and (13) treating a subject with a condition associated with an interaction of an RAGE with a receptor for RAGE on a cell. The methods can be used for treating conditions associated with an interaction of an ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzhelmer's disease, senility, renal failure, hyperlipidaemic atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia associated with head trauma, amyotrophic lateral syndrome, dementia associated with head trauma, periodontal disease, neuropathy, retinopathy, nephropathy wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
                                                                                                                                        Sequence
                                                                                                                                                                              or neuronal
                2
QNITARIGE 10
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                                                                                                                                                                              degeneration.
                                                  Conservative
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                                                                   91.7%;
                                                    0;
                                                                     Score 44;
Pred. No.
                                                    Mismatches
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Search completed: April 24, 2002, 09:17:37 Job time: 141 sec

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Perfect score:
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        score q
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seq length: 2000000000
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000 Co
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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US-08-633-148-4
US-08-633-148-2
US-08-241-766-6
US-08-241-766-6
US-08-241-766-7
US-08-802-141-4
US-08-802-141-4
US-08-93-12-157-10
US-08-793-035-9
US-08-794-711A-1
US-08-704-711A-1
US-08-704-711A-1
US-08-704-711A-2
US-08-483-899-1
US-08-487-157-16
US-08-487-173-16
US-08-487-173-16
US-08-487-173-16
US-08-487-173-16
US-08-487-173-16
US-08-615-271-16
US-08-615-271-16
US-09-074-659-16
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6.958 Million cell updates/sec
Sequence 12, Appl
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Sequence 14, Appli
Sequence 16, Appli
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ALIGNMENTS	US-09-106-467-16 US-08-673-814-6 US-08-93-359-24 US-08-989-358A-2 US-08-989-358A-2 US-08-989-318-4 US-09-074-658-21 US-08-277-231A-4 US-08-477-326-7 US-08-477-326-7 US-08-477-326-7 US-08-477-5941-20 US-08-867-941-27 US-08-867-941-27 US-08-312-157-6 US-09-312-157-6 US-09-312-157-8 US-09-312-157-8 US-09-312-157-8 US-09-312-157-8 US-09-312-157-8 US-09-312-157-8 US-09-312-157-8 US-08-867-941-13
	Sequence 16, Appli Sequence 24, Appli Sequence 2, Appli Sequence 2, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 20, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 13, Appli Sequence 13, Appli

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US-08-633-148-12
                                                                                                                                        ; MOLECULE TYPE: peptide US-08-633-148-12
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GENERAL INFORMATION:
                                                   Matches
                                                                     Query Match
Best Local
                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/633,1.
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAGASHIMA, MARCH APPLICANT: HOLLANDER, DORIS A.
APPLICANT: HOLLANDER, DORIS A.
APPLICANT: HOLLANDER, DORIS AND GENERATION
TITLE OF INVENTION: ENTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOMOSEND & TOMNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MORSER, MICHAEL J.
· 1 AQNITARIGE 10
                                                   Local Similarity nes 10; Conserv
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TOPOLOGY: 11
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                                                    Conservative
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                                                                   Score 48;
Pred. No.
                                                   Mismatches
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J.0003;
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US-08-633-148-18

Sequence 18, Patent No. 5

Application US/08633148

GENERAL INFORMATION:

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                                                                                                                                                                                                     Sequence 4, Application US/08633148 Patent No. 5864018
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                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
         CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148 FILING DATE: 16-APR-1996
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 014618-005600US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                      TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NACASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                     1 AQNITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                     AQNITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
10; Conserv
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SAN FRANCISCO
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                                                                                                                            MORSER, MICHAEL J.
NAGASHIMA, MARIKO
HOLLANDER, DORIS A.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                        mismatches 0;
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                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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                 INFORMATION FOR SEQ ID NO: 2:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MURCHY ESO., MATTHEW B.
REGISTRATION NUMBER: 39,787
REGISTRATION NUMBER: 014618-005600US
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MORSER, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: SAN FRANCISCO
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5. 5864018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAGASHIMA, MARIKO
HOLLANDER, DORIS A.
                                   (415) 326-2422
                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                       (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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RESULT 6
US-08-241-766-7
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US-08-241-766-6
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APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: deLISLE, G. W.
APPLICANT: deLISLE, G. W.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: AND TRE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/241,766
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                           Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1018
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AQNITARIGE 32
                                                                75 ADRITATIGE 84
                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AQNITARIGE 10
                                                                                    1 AQNITARIGE 10
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                                                                                                                                                                                                                                                                         269 amino acids
                                                                                                                             Conservative
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                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                           6:
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                                                                                                                                              Score 32;
Pred. No.
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Pred. No. 0.01;
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                                                                                                                                                             DB 1;
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                                                                                                                                                             Length 269;
                                                                                                                             Indels
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US-08-802-141-4
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                       Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/241
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: deliste, G. W.
APPLICANT: deliste, G. W.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inha AGENT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                       TITLE OF INVENTION: ROTTITLE OF INVENTION: CONNUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acid
                                                                                                                                                                                          APPLICANT: GLASS, ROGER I.
APPLICANT: GENTSCH, JOHN R.
APPLICANT: BHAN, M. K.
APPLICANT: DAS, BIMAL K.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: /J.
                                                  STREET: 127 Pe
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 494-0792
                  COUNTRY: USA
ZIP: 30303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AQNITARIGE 10
                                                                                                                                                                                                                                                                                        , Application US/08802141 5773009
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                                                  Georgia
                                                                                       127 Peachtree
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                                                                                                      NEEDLE & ROSENBERG,
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                                                                                                                                                           COMPOSITIONS
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70.0%;
                                                                                                                                                                           ROTAVIRUS STRAIN AND RELATED
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                                                                                                      P.C.
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22;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

MEDIUM TYPE:

Floppy disk

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Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-434-000A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08434000A Patent No. 6046037
                                                            PRIOR APPLICATION DATA: i
PRIOR APPLICATION DATA: i
PRIOR APPLICATION DATA: d
APPLICATION NUMBER: 08/
FILING DATE: 12/30/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 688-9880
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: IBM P.C. SOFTWARE: WORD Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Dis
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFÓRMÁTION:
NAME: Gulse, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.609
                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                          STREET: 633 West F
                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                 FILING DATE:
                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 ENVTVQIGE 39
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                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                9007
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633 West Fifth Street
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                                                                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                             IBM Compatible
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55.6%;
                                                                                                                                                                                                                                                                             Diskette, 1.44 Mb
                                                                          1: including application
1: described below:
08/367,395
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                                                                                                                                                                               US/08/434,000A
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Pred. No.
                                                                                                                                                                                                                              DOS 5.0
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DESCRIPTION: R. SEQUENCE DESCRIPTION: SEQ ID NO: US-09-312-157-10
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US-09-312-157-10
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Best Local Similarity ///-
----hes 7; . Conservative
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                                                                                                                                                        SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 QNATAVIGE 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QNITARIGE 10
                                                                                                                                                                                           NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
PILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 769 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDREW C. HIATT, JULIAN

K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/312,157 FILING DATE: 14-May-1999 CLASSIFICATION: <Unknown>
                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suite 4700
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77.8%;
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                           Rat Polyimmunoglobulin Receptor : 10:
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Query Match
Best Local Similarity
Tatches 5; Conserv?
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US-08-793-035-9
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Best Local Similarity
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RESULT 11
US-08-793-035-10
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                                                                                                                                                                                                                                                                                     TELEFAX: 713.787.1440 INFORMATION FOR SEQ ID NO: 9:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0: FILING DATE: 28-JUL-1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
TITLE OF INVENTION: Brassica Napus
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 713.787.1400
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
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                                                           256 ASDMTAKLGE 265
                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9414622.2 FILING DATE: 20-JUL-1994
                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                              TOPOLOGY:
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                                                                                         1 AQNITARIGE 10
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                                                                                                                                                                                                                                                                                                                                                                             Kammerer, Patricia A.
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                                                                                                                                                                                                                                         amino acid
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Chase, Dianne
                                                                                                                                                                                                                                                       315 amino acids
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                                                                                                                       Conservative
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SYSTEM: PC-DOS/MS-DOS
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77.8%;
                                                                                                                                    62.5%;
50.0%;
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                                                                                                                                    Score 30; Pred. No.
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Pred. No. 1
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Best Local Similarity
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                                                                                                                                                                      Sequence 1, Application US/08704711A Patent No. 6114159
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08793035 Patent No. 6011201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 941
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/0
FILING DATE: 17-JUL-1995
ATFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                           APPLICANT: WILL, HOTST
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
STREET: 3000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                       256 ASDMTAKLGE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino a
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713.787.1440
713.787.1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/793,035 FILING DATE: 28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                           3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chase, Dianne
Elborough, Keiran
Fentem, Phillip A.
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White, Andrew
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                  62.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-Ketoacyl ACP Reductase Genes From
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                                                                                                                                                                                                                                                                                                                                                                  Score 30; Pred. No.
                                                                                                                                                                                                                                                                                                                                                  ced. No. 72;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Length 315;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

20007-5109

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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Best Local Similarity
5; Conserve
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Sequence 2. Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY:
US-08-704-711A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
         COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                               APPLICANT: WILL, HOTST
APPLICANT: HINZMANN, Bernd
APPLICANT: HINZMANN, BERND
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-MAR-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 4438838.1 FILING DATE: 21-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 QNYTPKVGE 134
                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                    STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 579 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE 4409663.1 FILING DATE: 17-MAR-1994
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CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                   TRY: USA
20007-5109
                                                                                                                                                                                                        D.C.
                                                                                                                                                                                                                                     3: Foley & Lardner
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55.6%;
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                         Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 579;
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RESULT 15
US-09-211-704A-9
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Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-08-448-489-1
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                                                                        Sequence 9, Application US/09211704A Patent No. 6271014
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SEIKI, Motcharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08448489 Patent No. 6184022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de Saint-Vis, Blandine Marie
APPLICANT: FOSSIEZ, Francois
APPLICANT: Caux, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
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APPLICANT:
                                                                                                                                                                       129 QNYTPKVGE 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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REFERENCE/DOCKET NUMBER:
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(202)672-5399
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55.6%;
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                                                                                                                                                                                                                                 Score 30; DB 4; NC
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                Length 582;
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NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPHONE: (650)852-9196
TELEPHONE: (650)496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-211-704A-9
Search completed: April 24, 2002, 09:18:16 Job time: 175 sec
                                                                                                           рь
                                                                                                                                                 Qy
                                                                                                                                                                                          Query Match 62.5%; Score 30; DB 4; Length 582; Best Local Similarity 55.6%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 09/005,263
FILING DATE: 09-CAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MA
TITLE OF INVENTION: an
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                           129 QNYTPKVGE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                    2 QNITARIGE 10
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                                  Post-processing:
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                                                                  DB seq
                                                                    length: 2000000000
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                                   Minimum Match 0%
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48
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        219241 seqs, 76174552 residues
                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                             AQNITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                    Compugen Ltd
                                                                                                                                                                                                                                                                                                            (without alignments)
19.678 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pir2:\*
pir3:\* Database

PIR\_68:\*

pir1:\*

## SUMMARIES

No.	Score	Match 100.0	Length	DB	<b>⊢</b> .	Description
2	44		402	N	906	Φ 1
ω	40	•	. 416		287	
4	36	٠	879		E69792	Ω.
տ	35	•	547		T29567	hypothetical
6	34	70.8	391		в83203	alginate o-acetyl
7	34	•	808		E64492	
œ	34		1155		H71456	probable pyrolysi
ø	34	•	1180		A35854	
10	33	•	223		H64065	mutator muth
11	ω u		387		G84190	
12	33	•	437		164114	nifs protein
13	33	•	486		E42902	Ω.
14	33		550		T06379	SAR DNA-binding
15	33	•	560		T06377	
16	33	•	792		в82752	۳.
17	33	•	4436		E71086	hypothetical
18	32	•	435		T01805	hypothetica
19	32	•	439		T01807	hypothetica
20	32	•	468		H69133	argininosucc
21	32	66:7	508		T50180	nucleolar
22	32	66.7	625		T16777	hypothetical
23	32	66.7	772		A46110	
24	32	66.7	941		$\frac{\omega}{\omega}$	
25	32	66.7	1160		DJEC3A	outer capsid prote probable chromosom
26	32	66.7	1160		A45915	cap ble irec
27	32	66.7	1160		885503	cap ble ired
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64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6
507	494	418	380	354	354	318	286	286	268	262	250	240	218	215	206
2	Ŋ	N	N	N	N	N	N	1	N	N	N	N	N	N	N
T20966	D86493	D75283	T04343	B85647	B47065	E70117	JN0816	C35124	D29826	T47002	C70869	E81261	в83396	JC5483	A64402
hypothetical prote	polymorphic outer	hypothetical prote	L-ascorbate oxidas	hypothetical prote	phosphate starvati	membrane fusion pr	2,6-dioxo-6-phenyl	2,6-dioxo-6-phenyl	hypothetical 28.8K	hypothetical prote	hypothetical prote	probable ABC trans	probable CoA trans	ABC-type transport	probable phosphati

## ALIGNMENTS

R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; M Genomics 23, 408-419, 1994 A;Title: Three genes in the human MHC class nterpart of mouse mammary tumor gene int-3. A;Reference number: A55562; MUID:95137587 N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot C;Species: Homo sapiens (man) C;Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999 C;Accession: I61596; B42879; S27968 A; Reference number: A; Accession: I61596 advanced glycosylation end-products receptor precursor - human T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, III region near the junction with the cla

A; Molecule type: DNA A; Residues: 1-404 < RES> A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/

J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for A;Accession: B42879
A;Molecule +---GB:D28769; NID:g561657; PIDN:BAA05958.1; PID:g561659 advanced glycosylation

A;Molecule type: mRNA A;Residues: 'G', 2-99','R',101-404 <NEE> A;Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846 A; Experimental source: lung

A; Note: sequence extracted from NCBI backbone (NCBIP:109438)

C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

A; Gene: GDB: AGER

A;Cross-references: GDB:306354; OMIM:600214 A;Map position: 6p21.3-6p21.3 A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2

A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG> F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT F;23-344/Domain: extracellular #status predicted <EXT> F;31-101/Domain: immunoglobulin homology <IM1>

F;345-362/Domain: transmembrane \*status predicted F;363-404/Domain: intracellular \*status predicted F;137-210/Domain: immunoglobulin homology <IM2>
F;252-303/Domain: immunoglobulin homology <IM3>

F; 25, 81/Binding site: carbohydrate (Asn) (covalent) #statu, 259-301/Disulfide bonds: #status predicted (covalent) #status predicted

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A;Mab position: 17
A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2 C;Superfamily: advanced glycosylation end products receptor; immunoglobulin hc C;Keywords: receptor; transmembrane protein F;31:100/Domain: immunoglobulin homology <IMM>
                             A; Molecule type: protein
A; Residues: 23-24, 'X', 26-37, 'X', 39-49, 'XX', 52-54 <SCH>
A; Reparimental source: endothelial cells
A; Note: sequence extracted from NCBI backbone (NCBIP:10)
C; Comment: Advanced glycosylation end products are hetcellular function, thus contributing to tissue lesions
                                                                                                                                                                                                A:Note: sequence extracted from NCBI backbone (NCBIP:109436)
A:Note: parts of this sequence, including the amino end of the mature protein, were dete R:Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He J. Biol. Chem. 267, 14987-14997, 1992
J. Biol. Chem. 267, 14987-14997, 1992
A:Title: Isolation and characterization of two binding proteins for advanced glycosylatians R:Reference number: A42878; MUID:92340546
A:Reference number: A42878; MUID:92340546
A:Adcession: A42878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: \bar{1}-402 < ROW> A; Cross-references: EMBL: AF030001; NID: g2564945; PID: g2564950 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-416 <NEE>
A;Croos-references: GB:M91212; NID:g163650; PIDN:AAA03575.1;
A;Experimental source: lung
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A;Title: Cloning and expression of a cell surface receptor for advanced glycosylat A;Reference number: A42879; MUID:92340547
A;Accession: A42879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: A42879; A42878; S27949
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C;Accession: T09062
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A; Accession: T09062
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A;Description: Sequence of the mouse major histocompatibility locus class III region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable advanced glycosylation end-products receptor precursor - N; Alternate names: RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     advanced glycosylation end-products receptor precursor - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                             Note: sequence extracted from NCBI backbone (NCBIP:109434); Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosyllular function, thus contributing to tissue lesions in diabetes.
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nes 9; Conserv
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100.0%;
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Pred. No.
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Pred. No. 0.021;
Mismatches 0
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  the effects of amyloid beta peptide on
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hypothetical protein C44C1.4 - Caenorhabditis elegans C;Specles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T29567
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T29567
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Query Match Best Local : Matches

Similarity 6; Conser

Conservative

75 66

Score 36; DB Pred. No. 19; 2; Mismatches

Length 879;

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45

#sequence\_revision 15-Oct-1999 #text\_change

2 QNITARIGE

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C:Accession: E69792
C:Bron, S:, Brouillet, S:, Bruschi, C.V.; Caldwell, B:, Capuano, V.; Carter, N.M.;
C:Bron, S:, Brouillet, S:, Bruschi, C.V.; Caldwell, B:, Capuano, V.; Carter, N.M.;
A:, Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamako, T.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtill
A; Reference number: A69580; MUID: 98044033
A; Statius: preliminary: nucleic acid sequence of the Gram-positive bacterium Bacillus subtill
A; Reference number: A69580; MUID: 98044033
A; Experimental C; Genetics: A; Gene: yeeA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ates in the neurotoxic pathway that produces dementia in Alzheimer's disease. C;Function:
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-416/Product: advanced glycosylation end-products receptor RAGE #status predicted F;31-354/Domain: extracellular #status predicted <EXT>
F;3-354/Domain: immunoglobulin homology <IM2>
F;136-209/Domain: immunoglobulin homology <IM3>
F;136-213/Domain: immunoglobulin homology <IM3>
F;262-313/Domain: immunoglobulin homology <IM3>
F;262-313/Domain: immunoglobulin homology <IM3>
F;262-313/Domain: immunoglobulin homology <IM3>
F;362-313/Domain: immunog
                                                                                                                                                                A; Residues: 1-879 < KUN>
A; Cross-references: GB:
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence
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8; Conser
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                                                                                                              GB:Z99107; GB:AL009126; ce: strain 168
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R;Bradshaw, H.; Stellyes, L.

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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
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R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:C44C1.4
A;Introns: 31/3; 98/1; 119/3; 178/2; 343/3; 373/3; 404/3; 440/2; 481/2; 531/2
C;Superfamily: vacuolar protein sorting protein VPS45
                                                                                                                                                                                                                                                       hypothetical protein MJ1542 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999 C;Accession: E64492
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A;Reference number: A82950;
A;Accession: B83203
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A; Residues: 1-547 <BRA>
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                                             A; Molecule
                                                                                A; Reference number: A64300; A; Accession: E64492
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                                                             A;Status: preliminary; nucleic acid sequence
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  GB:U67595;
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GB:L77117; NID:g1592170; PIDN:AAB99570.1; PID:g1500434;
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A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-1180 <IGN>
A:Cross-references: GB:X52140; NID:g56493; PIDN:CAA36384.1; PID:g56494
C:Superfamily: unassigned collagens; von Willebrand factor type A repeat
C:Keywords: cell adhesion; cytoskeleton; transmembrane protein
F:170-345/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                              C;Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 20-Sep-1999 (;Accession: A35854; S11243 R:Ignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F. J. Cell Biol. 111, 709-720, 1990 A;Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor A;Reference number: A35854; MUID:90338125
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Best Local Similarity
"hes 5; Conserv
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C;Keywords: hy
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A; Residues: 1-1155 < KAW>
A; Cross-references: GB: AP000001; NID: g3236128; PIDN: BAA29383.1;
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R;Kawarabayasi, Y.; Sawada, M.;
Time v : Funahashi, T.;
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C;Accession: H71456
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C; Species: Pyrococcus horikoshii
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                                     Query Match
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                                     Score 34; DB Pred. No. 72; 1; Mismatches
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Yamazaki,
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A; Accession: H64065
A; Status: nucleic acid
A; Molecule type: DNA
A; Residues: 1-223 <TIO
nifs protein homolog HI1295 - Haemophilus influenza C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 C;Accession: I64114; T09423 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayto
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A; Title: Genome sequence of Halobacterium species NRC-1
A; Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng0310c [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 *sequence_revision 02-Feb-2001 *text_change 16-Feb-2001 C;Accession: G84190 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.; Leithauser, B.; Keller, K.; Leithauser, B.; K
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C; Superfamily: cr
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A; Molecule type: DNA
A; Residues: 1-387 <STC
A; Cross-references: GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                            147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-387 <STO>
rences: GB:AE004437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ke:
.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; North, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein MJ1249
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100.0%;
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                                                                                                                                 Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g10579939; PIDN:AAG18891.1;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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   O.; Clayton,
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18;
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                                                                #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387
   R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.D.;
   Kirkness, E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebhardt,
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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M.; Weidman,
Jen, N.S.M.
   Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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A; Gene:
C; Super:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, A;Title: Whole-genome random sequencing and ass A;Reference number: A64000; MUID:95350630 A;Accession: I64114
                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-437 <WI
                                                                                                                                                                                                                                                                                                                      A; Reference number: Z16667
A; Accession: T09423
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-437 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269, 496-512, 1995
                                                                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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                                                                                                                                                                             Gene: HI1295; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman,
                                                                                               Query Match
Best Local
385
                                       2 QNITARIGE 10
QNIALRVGE
                                                                             Similarity 6; Conser
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                                                                               Conservative
393
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                                                                                                  68.8%;
                                                                               1;
                                                                                             Score 33;
Pred. No.
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                                                                                 Mismatches
                                                                                                  дв
39;
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assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L.I.; Glodek, A.; Kelley, J.M.; Weidman J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
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2-hydroxymuconic semialdehyde dehydrogenase (EC 1.2.1.-) - Pseud C;Species: Pseudomonas putida C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change C;Accession: E42902; S18244; S23488 E42902 (EC 1.2.1.-) - Pseudomonas putida 11-May-2000

E.L.;

Ornston,

unpublished s.; Rekik, M.; Bairoch, A.; Neidle, results 1991, cited by Genbank

A;Reference number: A57135 A;Accession: E42902

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-486 <HAR>

A;Cross-references: GB:M64747; NID:g151718; PIDN:AAA26053.1; PID:g151725 R;Harayama, S.; Rekik, M.; Bairoch, A.; Neidle, E.L.; Ornston, L.N.

7540-7548, 1991

zoate dioxygenases.
A; Reference number: A41659; MUID:92041666 J. Bacteriol. 173, 7540-7548, 19 A;Title: Potential DNA slippage structures acquired during evolutionary divergence of.

A; Contents: annotation A; Note: Genbank cited this reference and reported

R;Horn, J.M.; Harayama, S.; Timmis, K.N. Mol. Microbiol. 5, 2459-2474, 1991 in the reference paper DNA sequennce with its translation

A; Title: DNA sequence determination of the A; Reference number: S18244; MOID:92167811 A; Accession: S18244

A; Molecule type: DNA

A; Residues: 1-486 < HOR> R; Neidle, E.L.; Hartnett,

Eur. J. Biochem. 204, 113-120, C.; Ornston, L.N.; -120, 1992 Bairoch, A.; Rekik,

M.; Harayama,

Ac

compared

with

conceptual translation

TOL plasmid

(pWW0) xylGFJ

genes

of.

Pseudom

A;Title: Cis-diol dehydrogenases encoded A;Reference number: S23477; MUID:92155191 A;Accession: S23488 bу the TOL pWW0 plasmid xylL gene and the

A; Molecule type: DNA A; Residues: 1-486 <NET> A; Cross-references: EMBL:M64747 A;Status: nucleic acid sequence not shown; translation not

nucleotide sequence was submitted 6 the EMBL Data Library, March 1992

Wed Apr

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C:Genetics:
A;Gene: xylG
A;Genome: plasmid TOL pWWO
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C;Keywords: oxidoreductase
C;Keywords: aldehyde dehydrogenase homology <ALD>
                                                                                                                                                                                                                             R:Hatton, D.; Gray, J.C.

Submitted to the EMBL Data Library, April 1998

A:Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to nucleo A;Reference number: Z15637

A;Reference T06377

A;Accession: T06377

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-560 <HATD

A;Residues: 1-560 <HATD

A;Residues: 1-560 <HATD
                                                                                                                                                                                                                                                                                                                                                                                 SAR DNA-binding protein-1 - garden pea C;Species: Pisum sativum (garden pea) C;Decies: Pisum sativum (garden pea) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Jun-2000 C;Accession: T06377
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
T06377
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A; Residues: 1-550 <HAT>
A; Cross-references: EMB
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A;Accession: T06379
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Hatton, D.; Gray, J.C. submitted to the EMBL Data Library, April 1998 A;Description: cDNA encoding a pea SAR DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pisum sativum (garden pea)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 02-Jun-2000
C;Accession: T06379
Вþ
                                ρy
                                                                                                                                                       A;Gene: SARBP-1
C;Superfamily: garden pea SAR DNA-binding protein
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Best Local S
Matches 6
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
281 APNLTAMVGE 290
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nes 6; Conservative
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| |||| ||
74 ADGITAREGE 83
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                  1 AQNITARIGE 10
                                                                    Conservative
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                                                                  Score 33; DB Pred. No. 51; 2; Mismatches
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Search completed: April 24, 2002, 09:19:04 Job time: 203 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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RAGE_RAT
RAGE_MOVIN
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NIFH_CLOCB
CSD_HAEIN
NIFH_CLOCB
CSD_HAEIN
NUCC_STRD7
XYLG_PSEPU
INHA_MYCAV
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Y412_ARATH
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8 haemophilus
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## ALIGNMENTS

RR	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	RN RT RA RR	RESULT RAGE_H ID R AC DT 0 DT 2 DT 2 DT 2 OC AC AC OC
SEQUENCE FROM N.A. (ISOFORM 2).  SEQUENCE FROM N.A. (ISOFORM 2).  Schuler A., Richards J., Gaillard H., Thompson A., Diener C.,  Schuler A., Huber G.;  Schuler A., Diener C.,  Schuler A., Huber G.,  Schuler A., Huber G.,	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Spies T., Hood L.;  Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.  [4]  SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.  Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,  Yamamoto H.;  "Molecular heterogeneity of the receptor for advanced glycation endproducts.";  Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  [5]	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  MEDLINE=95137587; PubMed=7835890;  Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  INOKO H., Ikemura T.,  "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3.";  Genomics 23:408-419(1994).	SEQUENCE FROM N.A. (ISOFORM 1).  TISSUE=Lung;  MEDLINE=92340547; PubMed=1378843;  Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  Elliston K., Stern D., Shaw A.;  "Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins.";  J. Biol. Chem. 267:14998-15004(1992).	LIT 1 LHUMAN STANDARD; PRT; 404 AA. Q15109; Q15279; Q9Y3R3; Q9H2X7; Q15109; Q15279; Q9Y3R3; Q9H2X7; Q15NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q0-AUG-2001 (Rel. 40, Last annotation update) ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS). AGER OR RAGE. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID-9606;

DP3A\_PASMU
M7\_LILHE
LIM1\_LILLO
LIM2\_LILLO
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KDGL\_PSEDE
IF34\_YEAST

schizosacch
rattus norv
pasteurella
lilium henr
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lilium long
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saccharomyc pseudomonas

8 arabidopsis 9 methanobact 3 human rotav 2 vibrio chol 3 escherichia 7 salmonella

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BLOI\_PSEAR

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Best Local Similarity
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Pfam; PF00047; 19; 2.
SMART; SM00408; IGc2; 1.
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SMART; SM00290; IG_MIC; 1
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Alternative splicing; Polymorphism.
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SUBCELLULAR LOCATION: TYPE I MEMBI
SECRETED (ISOFORM 2).
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
2 C2-LIKE AND ONE V-LIKE DOMAINS.
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LIGVILWQRRQRRGEERKAPENQEEEEBERAELNQSEEPEAG
ESSTGGP -> VSDLERGAGRTRRGGANCRLCGRIRAGNSS
PGPGDDGRPGDSRPAHWGHLVAKAATPRRGEEGPRKPGGRG
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IG-LIKE C2-TYPE DOMAIN.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RICECEPTOR FOR ADVANCED GLYCOSYLATION END PRODICED OR RAGE.
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-i- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
-products (Ace). These are Nomenzymatically glycosylated proteins
WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
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TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
2 C2-LIKE AND ONE V-LIKE DOMAINS.
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                                                                             CYTOPLASMIC (POTENTIAL).
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IG-LIKE C2-TYPE DOMAIN 1
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STRAIN-BALB/C; TISSUE-Lung;
MEDLINE=97368045; PubMed=9224812;
Renard C., Chappey O., Wautter M.P., Nagashima M.,
Morser J., Zhao L., Schmidt A.M., Scherrmann J.M.,
                                                                                                                                                                                                                                                               MGD;
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ADVANCED GLYCOSYLATION
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                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
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Q62151;
                                                                                                                 TRANSMEM
                                                                                                                           DOMAIN
                                                                                                                                                  CHAIN
                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                       EMBL; L33412; AAA40040.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Recombinant advanced glycation end in normal and diabetic rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR FOR ADVANCED
                                                                                                                                                                      [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPE
2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED RATE IN DIABETES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmacol.
                                                                                                                                                                                                                             IPR003600;
                                                                                                                                                                                                                         IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
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                                                                                                                                               domain;
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23 403
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              341
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Rodentia;
   42668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
NN END PRODUCT-SPECIFIC RECEPTOR
D GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                      Glycoprotein;
  ₩.
IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. . . ) (POTENTIAL.

N-LINKED (GLCNAC. . . ) (POTENTIAL.

N-LINKED (GLCNAC. . . ) (POTENTIAL.)
                                                                                                ADVANCED GLYCOSYLATION END PRODUCT-
SPECIFIC RECEEPOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403
                                                                                                                                                                      Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                        There are no
                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                            its content
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Wautier J.L.;
                                                                                                                                                                                                                                                                                                                    bу
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; Murinae; Mus
                       (POTENTIAL)
            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacokinetics
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                                                                                                                                                                                                                                                                                                                                         restrictions on
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RESULT
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                                                                                                                                                                                                                       InterPro: IPR003600; Ig_like Ffam; PP00047; ig; 2.
SMART; SM00408; IGc2; 1.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_MHC; 1.
                               DOMAIN
TRANSMEM
DOMAIN
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neeper M., Schmidt A.M., Brett J., Yan S.D., Wan Elliston K., Stern D., Shaw A.; "Cloning and expression of a cell surface recept glycosylation end products of proteins."; J. Biol. Chem. 267:14998-15004(1992).

-!- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED PRODUCTS (AGE). THESE ARE NONENZYMATICALLY G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAGE_BOVIN STANDARD; PRT; 416 AA. Q28173; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVIN
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                 SIGNAL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).
                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                   EMBL; M91212; AAA03575.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92340547; PubMed=1378843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGER OR RAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROT
TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN
2 C2-LIKE AND ONE V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RATE IN DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHICH ACCUMULATE IN VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                           1212; ....
; IPR003006; Ig_m...
); IPR003598; Ig_c2.
; r~~03600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
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100.0%;
                                                                                                                                                                                                              Glycoprotein; Transmembrane; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44;
Pred. No.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                         IG-LIKE V-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
                                                                                                                                    EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                POTENTIAL.
                                                                                                                          CYTOPLASMIC
                                                                                                                                                                    SPECIFIC
                                                POTENTIAL
                                                              POTENTIAL.
                                                                                                                                                                                  ADVANCED GLYCOSYLATION END PRODUCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                     RECEPTOR
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0.089;
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                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGING
                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUPERFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
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 (POTENTIAL)
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Best Local S
Matches 8
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E-R IN COLLAGEN.

1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1 ASSOCIATES WITH BETA-1.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTI-

WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.

1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99313197; PubMed-10386626;
Nolte M., Pepinsky R.B., Venyaminov S.Y., Koteliansky V.,
Gotwals P.J., Karpusas M.;
"Crystal structure of the alphalbetal integrin I-domain: insights into integrin I-domain function.";
FEBS Lett. 452:379-385(1999).
-i- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-COLLAGEN.
                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imodified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                   InterPro; IPR000413; Integrin_alpha InterPro; IPR002035; wWFA. Pfam; PF01839; FG-GAP; 5. Pfam; PF00357; integrin_A; 1. Pfam; PF00092; wa; 1.
                                                                                                                                                                                    EMBL; X52140; CAA36384.1;
PIR; A35854; A35854.
HSSP; P11215; 1A8X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90338125; PubMed=2380249;
Ignatius M.J., Large T.H., Houde M., Ta
Esch F., Carbonetto S., Reichardt L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAL_RAT STANDARD; PRT; 1180 AA.

p18614;
p18614;
p1-NOV-1990 (Rel. 16, Created).
p1-NOV-1990 (Rel. 16, Last sequence update)
p20-AUG-2001 (Rel. 40, Last annotation update)
INTEGRIN ALPHA-1 PRECURSOR (LAMININ AND COLLAGEN RECEPTOR) (VIA-1)
(CD49A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 151-364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITGA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
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|||||||:
| QNITARIGK 32
        '00092; vwa, _____PR00453; VWFADOMAIN.
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416
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     Int_alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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44182 MW;
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                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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ID MUTH_HAEIN
AC P44688;
DT 01.NOV-1995
DT 02.AUG-2001
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Similarity 6; Conserv

Conservative

Mismatches

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P44688; 01-NOV-1995 01-NOV-1995 20-AUG-2001

(Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)

STANDARD;

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Query Match
Best Local S
Matches 6
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SIGNAL
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1180
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            70.8%;
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FG-GAP 1.

FG-GAP 2.

VWFA.

FG-GAP 3.

FG-GAP 4.

FG-GAP 5.

FG-GAP 6.

FG-GAP 7.

POTENTIAL.

POTENTIAL.

POTENTIAL.

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POTENTIAL.

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GEFKR MOTIF

BY SIMILARITY.

           Score 34;
Pred. No.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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; Signal; Repeat; Calcium;
                                                                       (GLCNAC)
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                          Length 1180;
                                                                      (POTENTIAL)
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(POTENTIAL).
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 RESULT 7
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Best Local
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Q59270;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
        SEQUENCE FROM N.A.

STRAIN-ATCC 18532;
Chen T., Leschine S.B.;
Chen T., Leschine S.B.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FI
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 CO
IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32723; AAC22062.1;
HSSP; P06722; 2AZO.
TIGR; HI0403; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed 7542800;
                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; P. Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTUM
                                                                                                                                                           Clostridium
                                                                                                                                                                          NIFH.
                                                                                                                                                                                                    NITROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and
influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA MISMATCH
                                                                                                                   NCBI_TaxID=29355;
                                                                                                                                                                                    (NITROGENASE
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                                                                                                                                 lostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
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een the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                            ITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCES. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long
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(Rel.
(Rel.
IRON
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Conservative
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                                                                                                                                                           cellobioparum.
                                                                                                                                                                           (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
IRON PROTEIN (EC 1.18.6.1) (NITROGENASE COMPONENT
REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPAIR PROTEIN
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                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24906
                                                                                                                                                                                                                                                                                                                                                                                                             68.88;
                                                                                                                                             Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endonuclease; Complete proteome
306 MW; 339A4EF9DA0E622A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Pasteurellaceae;
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  REDUCED
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assembly of Haemophilus
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                                                                                                                                                                                                                                                                 AA
                                                                                                                                            group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
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                        FIXATION ARE COMPONENTS:
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                              SEQUENCE FROM / KW20;

STRAIN=RD / KW20;

MEDLINE=9535030; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Meddman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D., Wetchback T.R., Hanna M.C., Muyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Smith H.O., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSD_HAEIN STANDARD; PRT; 43/ MA. 057476; 005054; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE CYSTEINE DESULFURASE (EC 4.4.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended 
                                                 Science 269:496-512(1995).

Science 269:496-512(1995).

Science 269:496-512(1995).

FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR AND SELENIUM ATOMS FROM L-CYSTEINE, L-STEANOUSTEINE, AND L-SELENOCYSTEINE TO PRODUCE L-LAININE (BY SIMILARITY).

SELENOCYSTINE TO PRODUCE LAILANINE (BY SIMILARITY).

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. CSD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00142; fer4_NifH; 1.
PRINTS; PR00091; NITH_GORASEII .
PROSITE; PS00746; NIFH_FRXC_1; FALSE_NEG
PROSITE; PS00692; NIFH_FRXC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59414; HSSP; P00459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSD OR HI1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Nitrogen fixation; Iron-sulfur; 4Fe-4S; ATP-binding.
NP_BIND 8 15 ATP (POTENTIAL).
                                                                                                                                                                                                                                                    influenzae Rd
                                                                                                                                                                                                                                                       "Whole-genome random sequencing
influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae
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SIMILARITY: BELONGS TO THE NIFH/CHLL FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Chow K.T., Pope M.K., Davies J.E.;

Chow K.T., Pope M.K., Davies J.E.;

"Characterization of a vanillic acid non-oxidative gene cluster from Streptomyces.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ datab-i- INDUCTION: SYMTHESIZED IN RESPONSE TO VANILLATE-i- SIMILARITY: BELONGS TO THE UBID FAMILY.
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TIGR; HI1295; -.
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Pron; Pr00266; aminotran_5; 1.
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PROSITE; PS00595; AA_TRANSFER_CLASS_5; FALSE_NEG.
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Lyase; Pyridoxal phosphate; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol: 177:1196-1201(1995).

J. Bacteriol: 177:1196-1201(1995).

-i- FUNCTION: 2-HYDROXYMUCONIC ACID SEMIALDEHYDE CAN BE CONVERTED TO 2-HYDROXYPENT-2,4-DIENOAM'E EITHER DIRECTLY BY THE ACTION OF 2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (HMSH) OR BY THE ACTION OF THEEE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD. CAN OXIDIZ NOT ONLY 2-HYDROXYMUCONIC SEMIALDEHYDE AND ITS ANALOGS. OPTIMAL PH OF CATALYSIS FOR THE DENZALDEHYDE AND ITS ANALOGS. OPTIMAL PH OF CATALYSIS FOR THE OXIDATION OF 2-HYDROXYMUCONIC SEMIALDEHYDE AND BENZALDEHYDE ARE RESPECTIVELY 8.3 AND 9.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inoue J., Shaw J.P., Rekik M., Harayama S.;
"Overlapping substrate specificities of benzaldehyde dehydrogenase
(the xylC gene product) and 2-hydroxymuconic semialdehyde
dehydrogenase (the xylG gene product) encoded by TOL plasmid pwwO c
Pseudomonas putida.";
T pertectal 1777.
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PIR; S18244; S18244.
PIR; E42902; E42902.
PIR; S23488; S23488.
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"DNA sequence determination of the TOL plasmid
Pseudomonas putida: implications for the evolut
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                                                                                                                                                                                                       InterPro; IPR002086; Aldehyde_dehydr
                                                                                                                                                                                                                                  HSSP; P20000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRESOLS AND CATECHOL. PHENOL METABOLISM. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiol.
                                                                                                                                                                                 PF00171;
                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                PS00687; ALDEHYDE_DEHYDR_GLU; 1.
hydrocarbons catabolism; Oxidoreductase;
254 BY SIMILARITY.
288 288 BY SIMILARITY.
11 12 EL -> AF (IN REF. 3).
                                                                                                                           PS00070;
PS00687;
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01-NOV-1995
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ENOYL-[ACYL-C
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SEQUENCE
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH)
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Oxidoreductase; NAD; Fatty aci
NP_BIND 135 164 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GIR10;
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NCBI_TaxID=1764;
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                                                                                                                                                                                                                                                                                                                                                                                                    268 AA;
(Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
(CARRIER-PROTEIN] REDUCTASE [NADH]
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NP_BIND 136
VARIANT 94
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TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
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TROOLYED IN MYCOLIC ACID BIOSYNTHESIS.
TROOLYED IN THE RESISTANCE AGAINST THE ANTITUBERCULOSIS DRUGS ISONIAZID AND ETHIONAMIDE.
THE SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                            Dante M., Wamsley P., Gibson A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
                                                                                                                                       Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 48.8 KDA PROTEIN M021B04.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires alicense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banerjee A., Dubnau E., Quemard A., Balasubramanian V., Um K.S Wilson T., Collins D., de Lisle G., Jacobs W.R. Jr.; "inhA, a gene encoding a target for isoniazid and ethionamide Mycobacterium tuberculosis."; Science 263:227-230(1994).
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                                                                                                                       eurosids II; Brassicales;
NCBI_TaxID=3702;
                                                                                                                                                                                                  A_TM021B04.13
                                                                                                                                                                                                                                                                              004656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MEDLINE=94112548; PubMed=8284673;
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SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. COLUMBIA;
Dante M., Wamsley P., Gibson A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
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Interpro; IFR002687; Nop.
Pfam; PF01798; Nop; 1.
ProDom; PD004104; Nop; 1.
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RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Aldredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA McCougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA McConglete genome sequence of Methanobacterium thermoautotrophicum
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7156(1997).

3C -!- CATALYTIC ACTIVITY: L-ARGININOSUCCINATE - FUMARATE + L-ARGININE.
3C -!- CATALYTIC ACTIVITY: LAST STEP IN ARGININE BIOSYNTHESIS.
3C -!- SIMILARITY: BELONGS TO THE LYASE 1 FAMILY. ARGININOSUCCINATE LYASE
                                                                                                                                                                             Matches
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Best Local
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30-MAY-2000
30-MAY-2000
20-AUG-2001
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                                                                                                                                                                                                                                                                                 InterPro; IPR000362; Fumarate_lyase.

Pfam; pF00206; lyase_1; 1.

PRINTS; PR00145; DCRYSTALLIN.

PRINTS; PR00149; FUMRATELYASE.

PROSITE; PS00163; FUMARATE_LYASES; FALSE_NEG.

Arginine biosynthesis; Lyase; Complete proteo

SEQUENCE 468 AA; 52439 MW; 2DD1F7A65FB5DF
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE) (ASAL).
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
        protein search, using sw model
                                                                                                                                                                                                                                                                                       9:
10:
11:
12:
13:
14:
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                                                                                                                                                                                                   Match
                                                                                                                                                                                                             Query
                                                                                                                                                             100.0
91.7
77.1
                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_17:*
l: sp_archea:
       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-689-469-6
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         April 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQNITARIGE 10
                                                                                                                                                                                                                                                                                                                                   sp_phage: *
                                                                                                                                                                                                                                                                                                                                               sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                      sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                      sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                sp_archea: *
                                                                                                                                                                                                                                                                                                                                                                           sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                      sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                             sp_fungi:*
                                                                                                                                                                                                                                                                                       sp_unclassified: *
                                                                                                                                                                                                                                                                                               sp_vertebrate:*
                                                                                                                                                                                                                                                                                                       sp_virus:*
                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                           sp_plant:*
                                                                                                                                                                                                   Length
       342
4402
246
879
879
8547
8547
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8547
76
90
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90
91
459
459
1155
81155
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23.240 Million cell updates/sec
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                                                                                                                   2 040496
Q18609
                                                                                                                                                                    Q9Y3R3
L 035444
                                                                       Q9YWS9
Q51393
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030579
031504
                Q58937
058048
Q9TRQ1
                                                              Q9ZIC1
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                                                                                         Q73304
Q9WBE2
Q76444
                                                     091900
        Q9LE26
                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473505
Q9trq1 bos taurus
Q9le26 psilo+--
                                                           040496 human immun Q18609 caenorhabdi Q73304 human immun Q9wbe2 human immun Q76444 human immun Q9yws9 human immun Q51393 pseudomonas Q9zicl pseudomonas
                                                                                                                                       P71291 escherichia
030579 bacillus su
031504 bacillus su
                                 091900 human immun
030965 rhizobium l
Q58937 methanococc
                                                                                                                                                                    Q9y3r3 homo sapien
Q35444 mus musculu
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					32																				
6.	σ.	6.	6.	6.	66.7	6	6.	8	8	8.	8	8	8	8	8	8	8	8.	8	8	8	8	8.	8	8
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N	ν	N	N	N	N	10	10	_	G	N	10	N	10	<u>.</u>	N	N	Ν	N	N	N	N	N	N	N	N
Q9LAH3	Q9x6U5	Q9Z473	Q9AQM1	Q9S6L2	Q9F6U7	Q9LD87	Q9LE27	058659	Q25198	Q9PEZ4	065334	Q9A310	065335	Q9HSB6	Q9CBM1	Q56499	066361	066358	066349	066324	066293	066292	Q56489	64	Q56486
	Q9x6u5 brevibacter		Q9aqm1 pseudomonas	Q9s612 corynebacte	ы	7			Q25198 hydra atten		4	$\sim$	5	_		499		O66358 unidentifi	349	066324 unidentif	O66293 unidentifi	6292	489	Q56487 unidentifi	Q56486 unident
pacte	icter	acte	nonas	pacte	pides	ntia	od i um	cus	tten	fas	sativ	oter	sativ	teri	cteri	cifie	ifie	cifie	٠٠٠٠	ifie	cifie	۳.	ifie	ifie	tifie

## ALIGNMENTS

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RESULT
Q9Y3R3
                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                           InterPro; IPR003598; Ig_c2.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 19; 2.
SMART; SM00410; IG_2; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                  Signal;
SIGNAL
                                                                        SEQUENCE
                                                                                                                                                                                                                                                                               Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.; Schuler A., Huber G.; "CDNA cloning of a novel secreted isoform of the human Receptor for Advanced Glycation End products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Y3R3
Q9Y3R3;
                                                                                                                                                                                                                                      EMBL; AJ133822; CAB43108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAGESEC
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                     SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                 Receptor.
                                                                          342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                       23
                                                                                                     22
342
             100.0%;
                                                                          36193 MW;
                                                                                      POTENTIAL.
RECEPTOR FOR ADVANCED GLYCATION PRODUCTS.
Score 48; DB 4; Length 342; Pred. No. 0.058; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                        35DDF66A13E39B38 CRC64;
                                                                                                                                                                                                                                                                     AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
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Conservative

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Gaps

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Best Local S
Matches 9
                   Matches
                              Query Match
Best Local
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035444;
01-JAN-1998
01-JAN-1998
01-JUN-2001
                                                                      Schramm S., Duncan M., Allen E., Araujo R., Ap
Davis K., Federspiel N., Hyman R., Kalman S.,
Lashkari D., Lew H., Lin D., Namath A., Oefner
Davis R.W.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ
EMBL; U70214; AAB08689.1;
SEQUENCE 246 AA; 26806 MW; 93FBCA6B432BE37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
SIMILAR TO E. COLI YJHH.
                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00408; IGc2; 1.
|SMART; SM00410; IG_IKe; 1.
|PROSITE; PS00290; IG_MHC; UNKNOWN_1.
|SEQUENCE 402 AA; 42653 MW; DBFDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
ROWEN L., Mahairas G.,
Loretz C., Schmidt S.,
Submitted (OCT-1997) to
                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig;
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                 Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAGE.
                             Local
                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                         QNITARIGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQNITARIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF030001; AAB82007.1; -.
                   Similarity
7; Conserv
                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003598; Ig_c2.
IPR003600; Ig_like.
IPR003006; Ig_MHC.
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3 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                       91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ಕ
                             77.1%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qin S., Ahearn M.E., Dankers C., Lasky S.,
Tipton S., Traicoff R., Zackrone K., Hood L.;
o the EMBL/GenBank/DDBJ databases.
                                                                                                                Allen E., Araujo R., Aparicio A., Chung E., Hyman R., Kalman S., Komp C., Kurdi O.,
in D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05,
17,
                                                                                                                                                                                         gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                              0;
                   1;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                       Score 44;
Pred. No.
                             Score 37; I
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                       93FBCA6B432BE37D CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                DBFDC50A6C8CB902 CRC64;
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND MAJOR
                                                                                                                                                                                                                                                                  246
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                           DB
3.5;
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0.49;
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on update)
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                                                                                          databases
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                                       Length 246
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                   Indels
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                   0
                                                                                                                                                                                                                                                                                                                                                             0;
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                   Gaps
                                                                                                                                                                                                                                                                                                                                                             Gaps
                  0;
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RESULT
O31504
ID
O32504
O32504
O33504
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                           A Kunst F. Ogsawara N. Moszer I. Albertini A.M. Alloni G.,
A Azevedo V. Bertero M.G. Bessieres P. Bolotin A. Borchert S.,
A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
A Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Chim K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C., R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 6
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030579;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. C
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-18 TRPC2;

BOTRISS R, SCHOVETER R.;

BOTRISS R, SCHOVETER R.;

BUBHIT AF012532; AAB66474.1; -..

INTERPRO; IPR002052; N6_MTASE; UNK

SEQUENCE 879 AA; 101108 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O31504;
O31504;
O1-JAN-1998
O1-JAN-1998
O1-JUN-2001
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
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O'Reilly M., Ogawa K., Ogawa Pohl T.M., Portetelle D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Firmicutes;
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3 (TrEMBLrel.
L (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Clostridium group;
us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group;
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T., Scanlan F
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 Q18609;
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SEQUENCE
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Submitted (JUL-1997) to the
EMBL; Y14356; CAA74727.1; -.
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InterPro; IPR002052; N6_Mtase.
PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
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NCBI_TaxID=11676;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson &
Graxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mof contiguous nucleotide sequence from chromosome III of C
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EMBL; U36879; AAC55538.1;
InterPro; IPR000328; Env_(
InterPro; IPR000777; GP120
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MEDLINE-96263682; PubMed-8924250;
Douglas N.W., Knight A.I., Hayhur
Daniels R.S.;
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MEDLINE-94150718; PubMed-7906398;
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SEQUENCE 851
  STRAIN-RUS12; PubMed-7639968; MEDLINE-95367213; PubMed-7639968; Lukashov V.V., Cornelissen M.T., Goudsmit J., Papuashvilli M.N., Rytik P.G., Khaitov R.M., Karamov E.V., De Wolf F.; Rytik P.G., Khaitov R.M., Karamov E.V., De Wolf F.; "Simultaneous introduction of distinct HIV-1 subtypes into differlsk groups in Russia, Byelorussia and Lithuania."; AIDS 9:435-439(1955).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency
Viruses; Retroid viruse
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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PF00516; GP120; 1.
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es; Retroviridae;
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Mismatches
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Pokrovsky V.V.,
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Kravchenko A.V., Foley B., Morrison I.,
Cheingsong Popov R., Weber J.N.;
"HIV-1 gagD/envG recombinants in Russia
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                                                     Franklin M.J.,
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A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Smith K.A., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Tomplete genome sequence of Pseudomonas aeruginosa PAOI, an "Complete genome sequence of Pseudomonas aeruginosa PAOI, an "Opportunistic pathogen";

"L Nature 406:959-964 (2000).

"R EMBL; U50202; AAB09782.1; -.
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Matches 6
091900;
01-NOV-1998 (TrEMBLrel. 08, Cr
01-NOV-1998 (TrEMBLrel. 08, L/
01-JUN-2001 (TrEMBLrel. 17, L
ENVELOPE GLYCOPROTEIN (FRAGME
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Q9ZIC1;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXCDEOXYRIBONUCLEASE VII LARGE SUBUNIT (FRAGMENT).
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                                                                              091900
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"Genetic studies of thermoregulated genes in the psychrotrophic batterium Pseudomonas fluorescens: unexpected role of exonuclease
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MF0;
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D.J., Lagrou M.
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K., Lim R.M.,
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EMBL; AF056186; AAC61999.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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Submitted (SEP-1997) t
EMBL; AF022807; AAC464
HSSP; P02942; 1007.
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                                                                              SMART; SM
SMART; SM
SEQUENCE
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
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Rhizobiaceae;
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17; SM00304; HAMP; 1.
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